Index for Volume 57 (2008)

Syst. Biol. 57(6):957–986, 2008
Copyright © Society of Systematic Biologists
ISSN: 1063-5157 print / 1076-836X online
DOI: 10.1080/10635150802630959

1fin, 922
25fin, 922
289fin, 922
3genes, 930, 931
6fin, 922
A Bayesian Perspective on a Non-parsimonious Parsimony Model, John P. Huelsenbeck, Cécile Ané, Bret Larget, and Fredrik Ronquist, 406
A Comparative Study in Ancestral Range Reconstruction Methods: Retracing the Uncertain Histories of Insular Lineages, John R. Clark, Richard H. Ree, Michael E. Alfaro, Matthew G. King, Warren L. Wagner, and Eric H. Roalson, 693
A Justification for Reporting the Majority-Rule Consensus Tree in Bayesian Phylogenetics, Mark T. Holder, Jeet Sukumaran, and Paul O. Lewis, 814
A Likelihood Framework for Estimating Phylogeographic History on a Continuous Landscape, Alan R. Lemmon and Emily Moriarty Lemmon, 544
A Model-Based Approach to Study Nearest-Neighbor Influences Reveals Complex Substitution Patterns in Non-coding Sequences, Guy Baele, Yves Van de Peer, and Stijn Vansteelandt, 675
A Novel Test for Host-Symbiont Codivergence Indicates Ancient Origin of Fungal Endophytes in Grasses, C. L. Schardl, K. D. Craven, S. Speakman, A. Stromberg, A. Lindstrom, and R. Yoshida, 483
A priori directionality test, 554
A Rapid Bootstrap Algorithm for the RAxML Web Servers, Alexandros Stamatakis, Paul Hoover, and Jacques Rougemont, 758
A. aeolicus, 855
A. altissima, 798
A. angelinajolieae, 646
A. atomarius, 629, 632, 634, 639, 641, 642
A. australis, 330
A. caesium, 800
A. carpinifolium, 800
A. catus, 121
A. caudatum, 805
A. circinatum, 796, 804, 806
A. cissifolium, 805
A. confucii, 798
A. cotylalveus, 23
A. crataegifolium, 800
A. dawsoni, 398, 403
A. distylum, 800, 804
A. fabri, 796
A. fumigatus, 618
A. glabrum, 796, 800, 804
A. haselbachense, 805
A. heldreichii, 805
A. henryi, 805
A. kweilinense, 796
A. laurinum, 800, 804, 806
A. longicaulis, 695
A. lyrata, 481
A. macrophyllum, 796, 800, 805, 806
A. macrophyllum/A. caesium, 804
A. melas, 119
A. nebulosus, 119
A. negundo, 796, 800, 804, 805
A. nidulans, 618
A. nipponicum, 800
A. oryzae, 618, 624
A. osmontii, 805
A. pensylvanicum, 796, 800, 806
A. pensylvanicum/A. crataegifolium, 804
A. petraea, 478
A. pictum, 280
A. pilosum, 800, 804
A. polydentatus, 22, 23
A. pseudoplatanus, 800, 804, 805
A. rubrum, 796, 800, 806
A. rubrum/A. saccharinum, 804
A. saccharinum, 796, 800, 807
A. saccharum, 795, 796, 800, 804
A. spicatum, 796, 800, 805
A. spicatum/A. carpinifolium, 804
A. stellatus, 912
A. tataricum, 800
A. tegmentosum, 800, 804
A. thaliana, 469
A. trautvetteri, 805
A. tricolor, 695
A. vastus, 403
A. wardii, 796
A. weltoni, 17, 22, 24, 27
Abacion magnum, 922
Abalistes stellatus, 907
Abalistes, 906, 910–912, 916
Abbotii, 880, 885, 886
Abronia, 172
Acanthascus (Rhabdocalyptus), 391
Acanthascus dawsoni, 390, 392, 398, 403
Acanthascus, 395
Acanthaster planci, 906, 918
Acanthocyclops vernalis, 922
Acanthospartum, 279
Accounting for Phylogenetic Uncertainty in Biogeography: A Bayesian Approach to Dispersal-Vicariance Analysis of the Thrushes (Aves: *Turdus*), Johan A. A. Nylander, Urban Olsson, Per Alström, and Isabel Sanmartín, 257
Acer arcticum, 806
Acer circinatum, 800
Acer, 795–808
Acer/Dipteronia, 800, 804, 807

Acheta veletis, 889
Achimenes, 706
Achnatherum inebrians, 485
Acipenser, 116
Acoelocalyx brucei, 391, 395, 398, 402
Aconitum, 58
Acontias, 644
Acrochordus, 421
ACT, 874
ACTB, 577
Actinobacteria, analysis of, 835
Actinopterygii, 519
Adaptive radiation, 562
Adelolecia pilati, 143
Adenocarpus, 748
adh1, 478, 480
ADORA3, 500
ADRA2B, 500
ADRB2, 500
Aegilops, 365
Aeonium, 734, 744, 748
Aeschynanthus, 694, 695
Aesculus, 796, 798, 807, 808
Aetiocetus cotylalveus, 17, 21, 27, 34
Aetiocetus polydentatus, 17, 22, 34
Aetiocetus weltoni, 16–18, 21, 23, 24, 27–30, 34
Aetiocetus, 23, 27
AFLP, 347
Agathis australis, 330
Agathis, 330, 331
Aglaocetus patulus, 34
Aglaocetus, 23
Agorophius pygmaeus, 31, 34
Agorophius, 34
Agrostis hiemalis, 485
Agrostis tenuis, 485
Aguileta, G., Marthey, S., Chiapello, H., Lebrun, M.-H., Rodolphe, F., Fournier, E., Gendrault-Jacquemard, A., and Giraud, T., Assessing the Performance of Single-Copy Genes for Recovering Robust Phylogenies, 613
Agus fran, 735
Agus juba, 735
Agus petr, 735
Agustinii, 741
Aichryson, 744, 747
Ailanthus, 798, 807
Ailuronyx seychellensis, 564
Akaike information criterion (AIC), 42, 60, 76, 77, 84, 113
Akanthosuchus langstoni, 181
Albatus, 310
Albertarum pueri, 282
Albifrons, 537
Albula, 537, 538
Alectoria, 142
Alekseyenko, Alexander V., Lee, Christopher J. and Suchard, Marc A., Wagner and Dollo: A Stochastic Duet by Composing Two Parsimonious Solos, 772
Alfaro, Michael E., see Clark, John R., 693
Alfaro, Michael E., see Dornburg, Alex, 905
Ali, Farhan, see Meier, Rudolf, 809
Alignment accuracy, 656
Alligator mississipiensis, 173
Allodaposuchus precedens, 181
Allognathosuchus, 181
Allopauropus proximus, 922
Allophana, 143
Alpine, 58
Alpinobombus, 59
Alström, Per, see Nylander, Johan A. A., 257
Alternative phylogenies, 785
Alternative splicing evolution, 772
Altingia, 43, 55
Ambiortus, 188
AMBN, 15, 17, 18, 21, 25–27, 33, 34, 577, 579
Ambrosina bassii, 269, 271, 272, 276, 277, 284
Ambrosina, 271, 272, 276, 277, 279, 282
Ambystoma californiense, 645
Ambystoma tigrinum melanostictum, 561
Ameiurus brunneus, 118
Ameiurus catus, 118
Ameiurus melas, 118
Ameiurus natalis, 118
Ameiurus nebulosus, 118
Ameiurus pectinatus, 117, 119
Ameiurus platycephalus, 118
Ameiurus sawrockensis, 119
Ameiurus serracanthus, 118
Ameiurus, 116, 117, 121, 125–128
Ameloblastin (*AMBN*), 15
Amia, 116, 519, 520, 527, 531, 532, 537
Amino acid model, 367
  dimension reduction, 368
  conversion to codon model, 368, 369
  codon model equivalent to, 369, 370
Amniote, 179
Amorphophallus, 272
Amplified fragment length polymorphism (AFLP), 347
  DNA fingerprinting, 347
  technique, 347, 348
  automated scoring of , 350
  Sampling Strategy for, 350, 351
  Generation of Raw data, 351
  optimal scoring parameters using AFLP, 352
An Integrative Method for Delimiting Cohesion Species: Finding the Population-Species Interface in a Group of Californian Trapdoor Spiders with Extreme Genetic Divergence and Geographic Structuring, Jason E. Bond and Amy K. Stockman, 628
Anadenobolus, 644
Anartia, 235
Anas, 188, 481
Ancestral range reconstruction, 693
  explicit methods, 698
  analysis, 699–701
Ancestral state reconstruction, 141
  of discrete morphological characters, 145, 146
  for deep nodes with high support, 146
  algorithm, 147
  using maximum parsimony, 149
  by SIMMAP, 152
Ancestral state reconstruction, 4
Amphidiscs, 400
Andersen 17, 34, 48, 91, 92, 143
Andersen, Heidi L., see Ekman, Stefan, 141
Androcymbium, 745, 747
Aneides flavipunctatus, 645
Anetia, 235
Anguilla, 537
Anidiops villosus, 645
Annelida, 514
Anolis auratus, 513
Anolis cristatellus, 573

Anolis extremus, 328
Anolis, 513, 571, 748, 889
Anomalous gene trees (AGTs), 131, 133, 134, 136, 139, 140
Anomalous gene trees, 131
Anomalous, 131, 132
Anomaly zone, 131, 132
Anomochilus, 430
Anopheles gambiae, 780
Anopsobius neozelanicus, 922
Anthoxanthum, 748
Anthus, 268
Anthyllis hermanniae, 279, 282
Antilocapra americana, 33
Antipathes galapagensis, 392
Antrodiaetus riversi, 645
Antrodiaetus unicolor, 644
Anura, 560
Ané, Cécile, see Huelsenbeck, John P., 406
Aoraki denticulate, 644
Apatornis, 200, 514
Aphanopetalum, 39, 43, 54
Apheliscus, 313
Aphredoderus, 538
Aphrocallistes vastus, 390, 403
Aphrocallistes, 391, 395, 396, 402
Aplysina fistularis, 392, 396
APOB, 500, 501
Apomastus, 644
Apomorphy, 903
APP, 500
Application of Phylogenetically Defined Names Does Not Require That Every Specifier Be Present on a Tree, Philip D. Cantino and Richard G. Olmstead, 157
Apsaravis, 188, 189
Apteronotus, 537
Aptostichus angelinajolieae, 641, 646
Aptostichus atomarius, 628–630, 634, 635, 639, 642, 643, 646
Aptostichus miwok, 641, 646
Aptostichus simus, 644
Aptostichus stanfordianus, 641, 646
Aptostichus stephencolberti, 628, 641, 646
Aptostichus stephencolberti, 628
Aptostichus, 629, 639, 641–644
Aptotichus angelinajoleae, 646
Aquifex aeolicus, 855
Arabidopsis halleri, 481
Arabidopsis thaliana, 469, 481, 780
Arabidopsis, 341, 478, 844
Araceae, 269
Arachnida, 931
Arbutus, 269
Archaea, 839
Archaeonycteris, 502
Archaeopteryx lithographica, 200
Archaeopteryx, 174–176, 185–187, 200
Archegozetes longisetosus, 711
Archeoziphius microglenoideus, 873
Argentina, 537
Argulus, 922
Argyranthemum, 734, 744, 748
Arisarum proboscideum, 283
Arisarum vulgare, 276
Arisarum, 271, 272, 276, 277, 282
Armadillidium vulgare, 922
Artemia salina, 922
Arthropoda, 920, 931
Arum maculatum, 276
Arum pictum, 269, 271, 272, 276, 277, 279–282
Arum, 271, 272, 276, 279, 280, 282, 283
Ascomycetes, 141
Ascomycota, 613
Ashbya gossypii, 615
Asher, Robert J., Geisler, Jonathan H., and Sánchez-Villagra, Marcelo R., Morphology, Paleontology, and Placental Mammal Phylogeny, 311
Asiatosuchus germanicus, 180
Asiatosuchus, 180, 181
Aspergillus fumigatus, 615
Aspergillus nidulans, 615
Aspergillus oryzae, 615, 616, 625
Aspergillus, 618, 624, 625
Aspidoscelis tigris, 421
Assessing the Performance of Single-Copy Genes for Recovering Robust Phylogenies, G. Aguileta, S. Marthey, H. Chiapello, M.-H. Lebrun, F. Rodolphe, E. Fournier, A. Gendrault-Jacquemard, and T. Giraud, 613
Assignment, 750
  graphic representation of, 753
  flowchart of, 751
  taxonomic, 752
  probabilities, 753
  false, 756
Astephus, 116, 117, 119, 126–128
Astragalus, 410, 414
Astraptes fulgerator, 207, 210, 212–214
Astrocystis, 155
Atolla vanhoeffeni, 392
atp1, 41
ATP7A, 17–19, 34, 500
AtpB, 41, 55, 56, 410, 414
Aulaxyper, 732, 733, 736, 740, 744, 745
Aulosaccus, 391, 395, 398
Australosuchus clarkae, 180
Automated scoring, 347
  parameter settings, 348
Avg(G), 767
AVG(P), 767
Avg(P), 767
Avg(R), 767
Avg(S), 767
Avise, John C., and Robinson, Terence J., Hemiplasy: A New Term in the Lexicon of Phylogenetics, 503
Axestotrigona ferruginea, 60
B. acutorostrata, 24
B. alboanalis, 72
B. appositus, 72
B. ashtoni, 73
B. atratus, 58
B. beaticola, 72
B. bimaculatus, 72
B. bohemicus, 73
B. borealis, 25, 72
B. brydei, 25, 34
B. californicus, 72
B. capriscus, 912
B. cingulatus, 72
B. conspicillum, 910, 916
B. dahlbomii, 68
B. davisii, 281
B. dispar, 281
B. distinguendus, 72
B. edeni, 34

B. ephippiatus, 58, 68
B. fernaldae, 73
B. fervidus, 72
B. flavidus, 73
B. fuscus, 912
B. gerstaeckeri, 58
B. handlirschi, 68
B. hypnorum, 71, 72
B. impatiens, 68
B. lapponicus, 72
B. lucorum, 71, 72
B. mexicanus, 68
B. monticola, 72
B. mori, 233, 235, 240
B. morrisoni, 58
B. musculus, 25
B. ovalis, 909
B. pensylvanicus, 72
B. perplexus, 71, 72
B. physalus, 25, 867, 873
B. polylepis, 912
B. pratorum, 71
B. pullatus, 58
B. sandersoni, 72
B. sitkensis, 72
B. sonorus, 58, 72
B. spinosus, 398, 909
B. sylvicola, 72
B. transversalis, 58
B. vetula, 912
B. volucelloides, 68
Bacchetta, Gianluigi, see Mansion, Guilhem, 269
Bacidia arceutina, 146
Bacidia heterochroa, 146
Bacidia rosella, 143
Bacidia, 145, 146, 150–154
Bacidina, 154
Bacillus, 840
Back-propagation, 202
  rule, 206
  neural network, 202, 203
  DNA barcoding, 202, 207
Bacterial Code, 507
Baele, Guy, Van de Peer, Yves and Vansteelandt, Stijn, A Model-Based Approach to Study Nearest-Neighbor Influences Reveals Complex Substitution Patterns in Non-coding Sequences, 675
Baker, C. Scott, see Dalebout, Merel L., 857
Balaena mysticetus, 23, 33, 34, 578
Balaena, 29
Balaenoptera acutorostrata, 16, 24, 30, 31, 33, 34, 574, 583
Balaenoptera bonaerensis, 25, 33, 34
Balaenoptera borealis, 33, 34
Balaenoptera brydei, 34
Balaenoptera davidsonii, 31
Balaenoptera edeni, 33, 34
Balaenoptera gastaldii, 34
Balaenoptera musculus, 25, 27, 33, 34, 867, 873
Balaenoptera omurai, 33, 874
Balaenoptera physalus, 16, 25, 31, 33, 34
Balaenoptera siberi, 32
Balaenoptera, 23, 25, 31, 32, 34
Balearica, 280
Baleen, 15
Balistapus undulates, 907
Balistapus, 906, 910, 912, 916
Balistes capriscus, 907
Balistes fuscus, 916
Balistes polylepis, 907
Balistes punctatus, 907
Balistes vetula, 907
Balistes, 909–912, 916, 918
Balistidae, 905
  phylogenetic relationships of, 916
Balistoides conspicillum, 906, 907
Balistoides viridescens, 906, 907, 910
Balistoides, 905, 906, 910, 912, 916
Balistomorphus orbiculatus, 909
Balistomorphus, 906
Ball, Bernard, see Regier, Jerome C., 920
Bandelt, Hans-Jürgen, and Fischer, Mareike, Perfectly Misleading Distances from Ternary Characters, 540
Baptornis, 187, 188
Barcoding, 750
Barrett, Paul M., see Wills, Matthew A., 891
Baru darrowi, 180
Basal centrality, 245
Basidiomycota, 613
Basilosaurus cetoides, 33
Basilosaurus, 30
Bathydorus spinosus, 398
Bathydorus, 391, 395
Baumgartner, Manuela, see Leigh, Jessica W., 104
Bayes factors (BFs), 120
Bayes factors, 388, 675, 795
Bayesian Analysis in Molecular Biology and Evolution (BAMBE), 87, 90
Bayesian analysis, 466
Bayesian Estimation of Species Trees (BEST), 299, 876
Bayesian genetic analyses, 732
Bayesian hierarchical model, 299
Bayesian inference, 86, 257, 693
Bayesian information criterion, 76
Bayesian methods, 905
Bayesian phylogenetic inference, 406, 772
Bayesian relaxed clock, 795
Bayesian, 708
  MCMC, 710
  constrained analysis, 714
  test results, 716
  unconstrained analysis, 713, 714, 716
Bayesian, 750
  framework, 750
  approach, 755, 756
BC, 507–512
BDNF, 17–19, 34, 500
Beiko, Robert G., Doolittle, W. Ford and Charlebois, Robert L., The Impact of Reticulate Evolution on Genome Phylogeny, 844
Belfiore, Natalia M., Liu, Liang, and Moritz, Craig, Multilocus Phylogenetics of a Rapid Radiation in the Genus *Thomomys* (Rodentia: Geomyidae), 294
Bell, Charles D., see Jian, Shuguang, 38
Bellemerea diamarta, 142, 143
Belodon, 177
Bencomia, 748
Benton, Michael J., see Martin, Jeremy E., 173
Beringian disjunctions, 795
Bernissartia fagesii, 181
Berta, Annalisa, see Deméré, Thomas A., 15
Betweenness, 432, 437
  Intermediary species and, 436, 437
  edge, 446
BF, 713

BGN, 874
Biarum dispar, 269, 271, 272, 276, 277, 279, 281
Biarum, 271, 272, 276, 279–281, 284
Biatora, 145
Biblis, 235
Bicirrhosum, 538
Bicyclus anynana, 232, 233, 241
Bicyclus, 235
Bilimbia sabuletorum, 143, 145
Bilimbia, 150–152
Billia, 796
Binary, 253
Bioclimatic modeling, 328
Biodiversity conservation, 825
Biodiversity conservation, 825
  applicability, 827
  stability, 826, 827
  bootstrapped, 849
  problem specification, 827, 828
Biogeography, 269, 795
Bit score, 219
BLAST database, 207
BLAST, 216
Boa, 538
Bombias, 68
Bombus gerstaeckeri, 75
Bombus luianus, 59
Bombus proavus, 59
Bombus s.s, 68
Bombus vetustus, 59
Bombus, 58–60, 62, 63, 66–75, 946
Bombyx mori, 231–233, 240–242
Bombyx, 235, 240
Bond sp. nov. (Figs. 1, 646
Bond, Jason E., and Stockman, Amy K., An Integrative Method for Delimiting Cohesion Species: Finding the Population-Species Interface in a Group of Californian Trapdoor Spiders with Extreme Genetic Divergence and Geographic Structuring, 628
Boomsma, Wouter, see Munch, Kasper, 750
Bootstrap support, 602
  survivor functions for, 608
  limiting distribution of, 604
Bordewich, Magnus, Rodrigo, Allen G. and Semple, Charles, Selecting Taxa to Save or Sequence: Desirable Criteria and a Greedy Solution, 825
Borealis, 25
Borealosuchus, 181
Bos taurus, 33, 574, 576–580
Bos, 577–580, 582
Boss, Darren, see Sanderson, Michael J., 335
Bothropolys multidentatus, 922
Botrytis cinerea, 615
Bottae, 310
Brachychampsa montana, 179, 181
Brachychampsa sealeyi, 180
Brachyelytrum erectum, 485
Brachyphona, 552, 560
Brachypodium sylvaticum, 485
Brachyrhinodon, 322
Branch Lengths, Support, and Congruence: Testing the Phylogenomic Approach with 20 Nuclear Loci in Snakes, John J. Wiens, Caitlin A. Kuczynski, Sarah A. Smith, Daniel G. Mulcahy, Jack W. Sites Jr., Ted M. Townsend, and Tod W. Reeder, 420
Branch length, 420
  related to clade support, 420
  estimation of, 421, 422
  correlation between bootstrap and, 425
  support/congruence and, 427
  estimation of , 429
  combined data, 429
Branchiopoda, 931
Branchiostoma floridae, 711
Brassica oleracea, 481
Brassica rapa, 481
BRCA, 500, 501
Breeding behavior, 474
Bridgeri, 310
Brimleyi, 552
Brintesia, 235
Bromham, Lindell, see Lanfear, Robert, 708
Bromus erectus, 485
Bromus purgans, 485
Bromus ramosus, 485
Brotula, 538
Brucei, 391
Bruen, Trevor C., and Bryant, David, Parsimony via Consensus, 251
Brumfield, Robb T., Liu, Liang, Lum, David E. and Edwards, Scott V., Comparison of Species Tree Methods for Reconstructing the Phylogeny of Bearded Manakins (Aves: Pipridae, *Manacus*) from Multilocus Sequence Data, 719
Bryant, David, see Bruen, Trevor C., 251
Brydei, 33, 34
BTN1A1, 577, 579, 588
Buchnera, 463
Bulgaria inquinans, 156
Bumblebees, 58
Burbrink, Frank T., and Pyron, R. Alexander, The Taming of the Skew: Estimating Proper Confidence Intervals for Divergence Dates, 317
Byssoloma leucoblepharum, 143
C-mos, 564
C. (L.) arboreus, 210, 211, 213
C. (L.) hiurai, 210, 211, 213
C. (L.) procerulus, 210, 211, 213
C. albicans, 790, 791
C. anthropophagorum, 695
C. arcticus, 398
C. aurantiicarpa, 695
C. baileyi, 465
C. californicus, 465
C. calpidicarpa, 695
C. coccinea, 695
C. compressa, 695
C. cordifolia, 695
C. dryas, 259
C. elegans, 935
C. eremicus, 465
C. feaniana, 695
C. formosus, 465
C. gracilirostris, 259
C. grandiflora, 695
C. grayana, 695
C. grayi, 695
C. hawaiensis, 695
C. hispidus, 465
C. intermedius, 465
C. jeffreyi, 259
C. jonesii, 695
C. kauaiensis, 695
C. kaulantha, 695
C. kealiae, 695
C. kusaimontana, 695

C. laxiflora, 695
C. leucantha, 695
C. lherminieri dominicensis, 259
C. lherminieri lawrencii, 259
C. longifolia, 695
C. meyeri, 398
C. milnei, 695
C. mollis, 707
C. munroi, 695
C. nukukivensis, 695
C. occidentalis, 259
C. occulta, 695, 704
C. ootensis, 695
C. pendula, 695
C. picta, 695
C. pogonantha, 695
C. propinqua, 695
C. pulchella, 695
C. richii, 695
C. samoensis, 695, 698, 699
C. sandwicensis, 695
C. spathulata, 695
C. sulcata, 695
C. thibaultii, 695
C. tintinabula, 695
C. urvillei, 695
C. ustulatus, 259
C. valdiviae, 398
C. viridis, 259
C. wagneri, 695
C. wainihaensis, 695
C. wawrae, 695
C. weddelli, 398
Cactophilus, 310
Caenorhabditis elegans, 780, 921, 926, 932
Caenorhabditis, 109, 921, 922
Caerulea, 470
Cairina moschata, 387
Calabaria, 429
Caladiosoma messelense, 276
Caladium, 272
Calamagras turkestanicus, 322
Calamagras, 327
Calamagrositis villosa, 485
Calculating gene tree probabilities (COAL), 133
Calibrations, 909
Calinaga, 237
Calla palustris, 272, 276
Callicarpa japonica, 707
Callithrix, 590
Calopadia foliicola, 143
Calycadenia, 705
Calycidium, 142, 156
Calymperaceae, 514
Cambrian explosion, 920
Camelus dromedarius, 33
Cameron, Sydney A., see Whitfield, James B., 939
Candida glabrata, 615
Candida lusitaniae, 615
Canis familiaris, 33, 574, 576
Canthidermis maculata, 912
Canthidermis maculatus, 907
Canthidermis, 906, 909–912, 916
Cantino, Philip D. and Olmstead, Richard G., Application of Phylogenetically Defined Names Does Not Require That Every Specifier Be Present on a Tree, 157
Cantino, Philip D., see Dayrat, Benoît, 503
Caperea marginata, 22, 23, 25, 26, 33, 34
Caperea, 25
Capitella species, 711
Carabus, 207, 210, 211
Carboxydothermus hydrogenoformans, 840
Carcinoscorpius rotundicauda, 922
Cardamine, 365
Carlia, 308, 560
Carolinensis, 391
Caryopteris, 514
Casarea dussumieri, 428
CAT, 874
Catalán, Pilar, see Díaz-Pérez, Antonio, 732
Catharus ustulatus, 561
Catharus, 259, 268
Cathayornis, 192
Catinaria atropurpurea, 143, 144
Catinaria, 153
Caulophacella, 391, 395, 398, 399, 402
Caulophacus (Caulodiscus), 391
Caulophacus (Caulophacus), 391
Caulophacus (Oxydiscus), 391
Caulophacus, 395, 398, 402
Cavia, 383
CBest-RBS, 767
CBest-SBS(GAMMA), 767
CBest-SBS, 767
CBest-SBS/CBest-RBS, 767
Cdx, 708, 712, 714, 715
Cedrela, 798
Cenozoic freshwater fishes, 116
Centris, 946
Cephaloleia, 59
Cercidiphyllum, 43
Cetaceans, 574
  OR subgenome of, 574
  relationships among, 580
Cetacean, 857
Cetotherium rathkii, 34
Cetotherium, 23
Cetradonia linearis, 142
Cetradonia, 156
Cetraria, 145
Chaetodipus, 449, 453, 454, 456, 457, 459, 465
Chaetomium globosum, 615
Chaetopterus variopedatus, 711
Chamaea fasciata, 644
Changchengornis, 188
Chanos, 537
Character evolution, 169
Character state reconstruction, 694
Character-state change, 195
Character-state space, 938
Charina, 429
Charlebois, Robert L., see Beiko, Robert G., 844
Chelicerata, 920
Chelonus, 940, 942
Chen, Duhong, see Sanderson, Michael J., 335
Chiapello, H., see Aguileta, G., 613
Chihuahuae, 310
Chilopoda, 931
Chirocentrus, 537
Chiroxiphia linearis, 725
Chiroxiphia pareola, 724
Chiroxiphia, 727

Chitoria, 235
Chlamydochaera, 259
Chlamydomonas, 108
Choeropsis liberiensis, 33
Chonecetus goedertorum, 17, 21, 23, 27, 34
Chonecetus, 23
Choneziphius, 873
Choristylis, 43
CHRNA1, 874
Chrysochloris, 315
Chrysops, 538
Chthalamus fragilis, 922
Cichlasoma, 533, 538
Cichlerminia, 263
Cichlherminia, 258, 259, 264
Citrinopsithyrus, 68
Clade assymmetry, 116
Cladistics, 179
Cladonia digitata, 143
Cladonia peziziformis, 143
Cladonia, 142
Clark, Clay, see McGowen, Michael R., 574
Clark, John R., Ree, Richard H., Alfaro, Michael E., King, Matthew G., Wagner, Warren L. and Roalson, Eric H., A Comparative Study in Ancestral Range Reconstruction Methods: Retracing the Uncertain Histories of Insular Lineages, 693
Clarke, Andrew C., see Holland, Barbara R., 347
Clarke, Julia A., and Middleton, Kevin M., Mosaicism, Modules, and the Evolution of Birds: Results from a Bayesian Approach to the Study of Morphological Evolution Using Discrete Character Data, 185
Clarke, Julia A., see Dayrat, Benoît, 503
Clarkia, 517
Clarkii, 549
Clathrochone clathroclada, 396, 402
Clathrochone, 391, 395, 398
Clathroclada, 391
Cluster analysis, 519
  data partitioning approach, 526
  parameter estimation, 522, 523
Cluster set, 338
Cluster Sets, 343
Clustering coefficient, 432
  units of co-occurrence and, 437, 438
  of a node, 438
CNGC5, 471, 473
CNR1, 500
Coalescence, 131
Coalescence, 466
  hybridization versus the sorting of ancestral polymorphisms tested by, 477–479
Coccidioides immitis, 615
Cochoa, 259
Coding Meristic Characters for Phylogenetic Analysis: A Comparison of Step-Matrix Gap-Weighting and Generalized Frequency Coding, A. Michelle Lawing, Jesse M. Meik, and Walter E. Schargel, 167
Codivergence in Heteromyid Rodents (Rodentia: Heteromyidae) and Their Sucking Lice of the Genus *Fahrenholzia* (Phthiraptera: Anoplura), Jessica E. Light and Mark S. Hafner, 449
Codon Model Equivalent to Amino Acid Model, 369
Codon model, 367
  conventional, 371–373
Coerulea, 467
Coevolution, 483
Cohesion species, 628
  concept, 629
  methodological framework to, 632
  topology-based evaluation of, 639–641
COI, 292, 564, 809, 810
COII, 292
Colias eurytheme, 233
Collar, David C., see Revell, Liam J., 591
Collembola, 220
Collins, Allen G., see Dohrmann, Martin, 388
Colonization of oceanic islands, 732
Colonization of South America, 264
Colossendeis, 923
Combinability, 469
Combination, 400
Commensalism, 840
Comparative method, 591
Comparison of Methods for Species-Tree Inference in the Sawfly Genus *Neodiprion* (Hymenoptera: Diprionidae), Catherine R. Linnen and Brian D. Farrell, 876
Comparison of Species Tree Methods for Reconstructing the Phylogeny of Bearded Manakins (Aves: Pipridae, *Manacus*) from Multilocus Sequence Data, Robb T. Brumfield, Liang Liu, David E. Lum, and Scott V. Edwards, 719
Compatibility, 251, 253
Concatenated analysis, 104
Concatenation with monophyly constraints (CMC), 876
Conchopetalum, 796
Concornis, 192
Condylostylus, 707
Confuciusornis, 189, 197
Congruence, 420
  analyses of support and, 422, 423
  gene tree, 428
Consensus method, 939
Consensus trees, 244, 785, 794
Conservation probability, 648
Consistent Estimation of Divergence Times in Phylogenetic Trees with Local Molecular Clocks, Bodil Svennblad, 947
Context effect, 675
Context-dependent evolution, 675
Conti, Elena, see Mansion, Guilhem, 269
Converged, 94, 95
Convolvulus, 747
Copepoda, 931
Cophocetus oregonensis, 34
Cophocetus, 23
Cophylogenetic methods, 449
  advantages and disadvantages, 450
  component of, 450
  data based, 452
Cophylogeny, 449
Cophylogeny, 449
  documentation of significant, 457
  test of, 456, 457
Coprosma propinqua, 280
Coptolabrus, 207, 214
CorrAll, 763
CorrBest, 763, 764
Coryphaenoides, 537
Cosmopolitan frog radiation, 327
Cospeciation, 449
  testing for codivergence and, 449, 450
  as contemporaneous speciation events, 460
Cotesia, 940
Covering property, 245
CP, 438, 439

CpG effect, 675
Craig, Timothy P., Evolutionary Ecology of Parasites, second edition, 182
Crambe, 734, 747
Cranoglanis bouderius, 118–120
Cranoglanis, 116, 126, 127
Cranston, Karen A., see Sanderson, Michael J., 335
Crassula, 43
Crateromorpha (Crateromorpha), 391
Crateromorpha meyeri, 398
Crateromorpha, 395, 402, 404
Cratogeomys merriami, 463
Cratogeomys perotensis, 450
Craven, K. D., see Schardl, C. L., 483
CREM, 500
Cretotrigona prisca, 60
Cretotrigona, 62
Crisp, Michael D., Ghosts of Gondwana: The History of Life in New Zealand, 329
Crocodylus niloticus, 173, 176–178
Crocodylus, 178, 181
Crocynia gossypina, 143–146
Crocynia, 150–152
Crotalus horridus, 172
Crown Clades in Vertebrate Nomenclature: Correcting the Definition of Crocodylia, Jeremy E. Martin and Michael J. Benton, 173
Crown groups, 841
Cryptococcus neoformans, 615
Cryptococcus, 156
Crypturellus, 192
Crysoleucas, 537
CSN2, 17–20, 34
Ctenolepisma lineata, 922
CTinter, 434
CTintra, 434
CTLA3, 874
Cuezzo, María Gabriela, see Santos, Daniel A. Dos, 432
Cummings, Michael P., see Regier, Jerome C., 920
Cunningham, Clifford W., see Regier, Jerome C., 920
Curimata aspera, 443
Curimata cerasina, 443
Curimata cisandina, 443
Curimata cyprinoides, 443
Curimata incompta, 443
Curimata inornata, 443
Curimata knerii, 443
Curimata macrops, 443
Curimata ocellata, 443
Curimata roseni, 443
Curimata vittata, 443
Curimata, 448
Curimatella dorsalis, 443
Curimatella lepidura, 442, 443
Curimatella meyeri, 443
Curimatella, 448
Curimatopsis crypticus, 443
Curimatopsis microlepis, 443
Curimatopsis myersi, 443
Cyanophora paradoxa, 686
Cyclamen balearicum, 280
Cyclamen, 283, 285
Cycles, 381, 383
Cylindrophis, 429
Cynomorium coccineum, 39
Cynomorium, 56
Cyphocharax aspilos, 442
Cyphocharax gangamon, 443
Cyphocharax gilbert, 442, 443
Cyphocharax gillii, 443
Cyphocharax gouldingi, 443
Cyphocharax laticlavius, 443
Cyphocharax leucostictus, 443
Cyphocharax meniscaprorus, 443
Cyphocharax mestomyllon, 443
Cyphocharax microcephalus, 443
Cyphocharax modestus, 443
Cyphocharax nagelii, 443
Cyphocharax nigripinnis, 443
Cyphocharax notatus, 443
Cyphocharax oenas, 443
Cyphocharax pantostictos, 443
Cyphocharax platanus, 443
Cyphocharax plumbeus, 443
Cyphocharax saladensis, 443
Cyphocharax spilotus, 443
Cyphocharax spiluropsis, 443
Cyphocharax stilbolepis, 443
Cyphocharax vanderi, 443
Cyphocharax vexillapinnus, 443
Cyphocharax voga, 443
Cypridopsis vidua, 922
Cypridopsis, 925, 927, 929
Cyrestis, 237
Cyrtandra richii, 707
Cyrtandra, 693–699, 701–707
Cyrtandra, 693
D. dyeriana, 796, 800, 804
D. heermanni, 450, 465
D. melanogaster, 935
D. merriami, 465
D. microps, 465
D. nelsoni, 465
D. ordii, 465
D. panamintinus, 465
D. persimilis, 308, 479, 480, 560, 730, 889
D. phillipsii, 465
D. rerio, 521
D. santomea, 481
D. simulans, 669
D. sinensis, 796, 800, 804
D. spectabilis, 465
Dactylurina, 60
Dakosaurus andiniensis, 176
Dalebout, Merel L., Steel, Debbie and Baker, C. Scott, Phylogeny of the Beaked Whale Genus *Mesoplodon* (Ziphiidae: Cetacea) Revealed by Nuclear Introns: Implications for the Evolution of Male Tusks, 857
Danio rerio, 791
Danio, 537
Daphnia, 220
Data for Evolution (DRIADE), 1
Data partitioning, 388, 519, 920
  rate variation, 393
  28S, 393
  dinosaur, 902
Dataset, 711
Dayrat, Benoît, Cantino, Philip D., Clarke, Julia A., and de Queiroz, Kevin, Species Names in the *PhyloCode*: The Approach Adopted by the International Society for Phylogenetic Nomenclature, 507
de Queiroz, Kevin, see Dayrat, Benoît, 503
Debaryomyces hansenii, 615

Decision theory (DT), 76, 77
Delphinapterus leucas, 33
Delphinidae, 574
Delphinus delphis, 576–578, 583, 588
Deméré, Thomas A., McGowen, Michael R., Berta, Annalisa and Gatesy, John, Morphological and Molecular Evidence for a Stepwise Evolutionary Transition from Teeth to Baleen in Mysticete Whales, 15
Dendrocrambe, 747
Dendroscope, 736
Denticrenatus, 22
Depressaria, 240
Deschampsia foliosa, 746
Descurainia, 267
Desmognathus fuscus conanti, 172
Desmognathus fuscus fuscus, 172
Developmental biology, 378
  analysis of, 379, 380
  evolution of, 380
Developmental sequences, 378
Deviacer wolfei, 806
Dhingra, Amit, see Jian, Shuguang, 38
Diapsida, 179
Diaulula sandiegensis, 513
Diaulula, 513
Dicamptodon aterrimus, 84, 560
Dicamptodon tenebrosus, 561
Dinosaurs, 891
  sample of, 899
  avian, 892
  nonavian, 899
Diorocetus hiatus, 34
Diorocetus, 23
Dioryctria, 645
Diplocynodon muelleri, 181
Diplocynodon ratelii, 180
Diplocynodon, 180
Dipodomys deserti, 451
Dipodomys ordii, 456
Dipodomys, 449, 452–454, 456, 457, 459, 460, 465
Dipteronia dyerana, 808
Dipteronia, 795–808
Dirichlet process prior, 671
Discodoridídae Diaulula sandiegensis, 513
Discodoridídae, 511, 513, 514
Disconcordant trees, 540
Discordance of Species Trees with Their Most Likely Gene Trees: The Case of Five Taxa, Noah A. Rosenberg and Randa Tao, 131
Discrete gamma categories, 141
Dispersal models, 732
  hypothesis testing of populations' IBD and, 742–744
  and the PCT, 745
  Bayesian approaches and, 746
Dispersal-extinction-cladogenesis (DEC), 6, 8, 11, 13
Dispersal-mediated allopatry, 693
Dispersal-mediated allopatry, 693
Dispersal-vicariance analysis, 257
Dispersal, 4
  explicit model of, 5
  rates of, 6
  between areas and rates of local extinction, 6, 7
  estimated rates for, 7
  history of the clade, 7
  constraints, 11
  unrealistic sequence of range evolution in, 13
DIVA, 269
Divergence of, 729
Diversification rates, 905
Divisestylus, 43, 52, 54, 55
DMP1, 16–18, 21, 26, 27, 33, 34
Dmp1, 33
DNA barcoding, 202, 216, 628
Dodonaea, 796
Does Choice in Model Selection Affect Maximum Likelihood Analysis?, Jennifer Ripplinger and Jack Sullivan, 76
Dohrmann, Martin, Janussen, Dorte, Reitner, Joachim, Collins, Allen G., and Wörheide, Gert, Phylogeny and Evolution of Glass Sponges (Porifera, Hexactinellida), 388
Domínguez, Eduardo, see Santos, Daniel A. Dos, 432
Doolittle, W. Ford, see Beiko, Robert G., 844
Doridina, 514
Dornburg, Alex, Santini, Francesco and Alfaro, Michael E., The Influence of Model Averaging on Clade Posteriors: An Example Using the Triggerfishes (Family Balistidae), 905
Dorosoma, 537
Dorudon atrox, 33
Dorudon, 30
Dot maps, 432
Double-membrane, 835
Doyle, Jeff J., see Maureira-Butler, Iván J., 466
DQA, 874
Dracophyllum, 330
Dracunculus muscivorus, 284
Dracunculus, 271, 272, 276, 279, 280, 282
Dromiciops gliroides, 315
Drosophila melanogaster, 240, 674, 780, 921, 926, 932
Drosophila pseudoobscura, 308, 479–482, 560, 730, 889
Drosophila simulans, 155
Drosophila yakuba, 481
Drosophila, 241, 373, 374, 478, 481, 589, 626, 645, 669, 674, 731, 857, 921, 922, 932, 938
Drosophila/Homo, 921
Dyeriana, 796
Dysidea etheria, 392
Dysidea, 392, 396
Díaz-Pérez, Antonio, Sequeira, Miguel, Santos-Guerra, Arnoldo and Catalán, Pilar, Multiple Colonizations, In Situ Speciation, and Volcanism-Associated Stepping-Stone Dispersals Shaped the Phylogeography of the Macaronesian Red Fescues (*Festuca* L., Gramineae), 732
E. argentina, 440, 441
E. australis, 578
E. coli, 214, 837
E. cryptomphala, 440, 441
E. escoipensis, 440, 441
E. glacialis, 23
E. guevarai, 440, 441
E. hemiclausa, 440, 441
E. hieronymi, 440, 441
E. jujuyensis, 440, 441
E. parodizi, 440, 441
E. puella, 440, 441
E. puntana, 440, 441
E. quirogai, 440, 441
E. rhathymos, 440, 441
E. saltana, 440, 441
E. tomsici, 440, 441
E. trenquelleonis, 440, 441
E. trifasciata, 440, 441
E. trigrammephora, 440, 441
E. tucumanensis, 440, 441
E. variegata, 440, 441

E. villavilensis, 440, 441
E. walshi, 440, 441
ear1, 482
Echiniscus viridissimus, 923
Echinopogon ovatus, 485
Echium, 734, 744, 747
Eco, 351, 734
Ecological interchangeability, 628
  second assessment of, 632
  evaluation of, 641, 642
Ecology and Evolution of Flowers, 516
Ecology and Evolution of Flowers, Jeff Ollerton, 516
Edeni, 25
Edwards, Scott V., see Brumfield, Robb T., 719
EF-1α, 920–923, 926, 931, 937
EF-2, 920–923, 926, 931, 937
Efficiency of Markov Chain Monte Carlo Tree Proposals in Bayesian Phylogenetics, Clemens Lakner, Paul van der Mark, John P. Huelsenbeck, Bret Larget, and Fredrik Ronquist, 86
Efficient algorithm, 345
Effigia okeefeae, 176
Eizirik, Eduardo, see Springer, Mark S., 499
Ekman, Stefan, Andersen, Heidi L. and Wedin, Mats, The Limitations of Ancestral State Reconstruction and the Evolution of the Ascus in the Lecanorales (Lichenized Ascomycota), 141
Elaphe obsoleta, 172
Elicodiceros muscivorus, 280
Elongation factor-1α, 878
Elops, 537
Elymnias, 240
Elymus canadensis, 485
Eminium koenianum, 283
Eminium, 271, 272, 276, 279, 283, 284
ENAM, 15, 17, 18, 21, 23, 25–27, 32–34
Enamelin (*ENAM*), 15, 32
Endeis laevis, 923
Endemism, 269
  Hercynian, 270, 271
  Mediterranean, 271
  Corsican, 280
  paleo-, 280
Endophytes, 483
Endosymbiotic gene transfer, 104
Eoalulavis, 188
Eocene extinction, 116
Eocetus wardii, 33
Eomysticetus whitmorei, 23, 27, 30, 34
Eomysticetus, 15
Eosuchus lerichei, 181
Eosuchus minor, 181
Epicephala, 463
Epichloë amarillans, 485
Epichloë baconii, 485
Epichloë brachyelytri, 485
Epichloë bromicola, 485
Epichloë elymi, 485
Epichloë festucae, 485
Epichloë glyceriae, 485
Epichloë sylvatica, 485, 497
Epichloë typhina, 485
Epichloë, 485
Epicrates, 32, 889
Epiperipatus biolleyi, 939
Epiphragmophora, 440, 441, 447
Equalrates Markov (ERM) model, 119, 161, 163, 165
Erebia, 240
Eremita, 263
Error rates, 347, 356
Error rates, 356
Eryx, 429
Escherichea coli, 826, 837
Eschrichtius robustus, 23
Eschrichtius robustus, 25, 26, 30, 33, 34
Eschrichtius, 25, 29
Eshanosaurus, 893, 901
Esox, 537
Estimating Evolution of Temporal Sequence Changes: A Practical Approach to Inferring Ancestral Developmental Sequences and Sequence Heterochrony, Luke B. Harrison and Hans C. E. Larsson , 378
Eubalaena australis, 33, 34
Eubalaena glacialis, 23, 33, 34
Eubalaena japonica, 33, 34, 576, 578, 583
Eubalaena, 23, 29, 34, 583, 586, 588
Eublepharus turkmenicus, 564, 566
Euchel:genes, 930, 934, 936
Euchelicerata, 931
Euglena, 220
Eulemur, 601
Eumesocampa frigilis, 922
EuMyPan:genes, 932, 934, 936
Euphorbia, 748
Euphractus sexcinctus, 317
Euplectella, 389, 391, 395, 398, 402, 403
Euproctus, 282
Eurycea, 514
Eurypauropus spinosus, 922
Eurytemora affinis, 922
Euthyneura, 514
Euxanthe, 235
Event-pairs, 378
  matrix, 378
  tracing of, 379
  cracking, 379
  tree, 384
Evidence for a New Root of the Tree of Life, James A. Lake, Jacqueline A. Servin, Craig W. Herbold, and Ryan G. Skophammer, 835
Evolutionary developmental biology, 378
Evolutionary Ecology of Parasites, 182
Evolutionary Ecology of Parasites, second edition, Timothy P. Craig, 182
Evolutionary lability, 591
Evolutionary Pathways, 184
Evolutionary simulation, 844
Evolution, 15
  of nutrient foramina and baleen, 27
  in Mysticeti, 21
Exiliboa, 429
Exons, 231
  finding and amplifying, 233, 234
  assessing long, 235
Explicit ancestral range reconstruction, 694
Extant phylogenetic bracket (EPB), 174
Extending subtree swapper (eSTS), 87, 91, 103
Extending tree bisection and reconnection (eTBR), 88, 91
Extinction, 4
F. agustinii, 732–747
F. boleni, 465
F. ehrlichi, 465
F. fairchildi, 450, 465
F. ferrisi, 465

F. francoi, 732–740, 742–746
F. Francoi, 738
F. hertigi, 458, 465
F. jubata, 732–742, 744, 745
F. microcephala, 451, 465
F. occa, 393, 394, 396
F. petraea, 732–740, 742–747
F. pinnata, 452, 465
F. reducta, 452, 465
F. rivularis, 732, 733, 744
F. rubra, 733
F. texana, 465
F. tribulosa, 465
F. zacatecae, 452, 465
Fagustinii, 744
Fabaceae, 466
Fagales, 807
Fagonia, 267, 917
Fahrenholzia, 449, 451, 453–458, 460, 463, 465
Falcago, 480
Farrea occa, 390, 396, 404
Farrea, 389, 391, 395
Farrell, Brian D., see Linnen, Catherine R., 876
Fellhanera bouteillei, 143
Fellhanera subtilis, 143
Female holotype, 646
Female paratype, 646
Fernández, Hugo R., see Santos, Daniel A. Dos, 432
Fervidobombus, 62, 68–70, 72, 74
Festuca agustinii, 733, 740
Festuca francoi, 741
Festuca jubata, 737, 739, 741
Festuca longifolia, 485
Festuca petraea, 741, 746
Festuca rubra, 485
Festuca, 732–738, 740–745, 747
Festuca sect. *Aulaxyper*, 732
Ficus, 463
Filter-feeding, 15
Filtered Z-Closure Supernetworks for Extracting and Visualizing Recurrent Signal from Incongruent Gene Trees, James B. Whitfield, Sydney A. Cameron, Daniel H. Huson, and Mike A. Steel, 939
Firmicutes, 835
Fischer, Mareike, see Bandelt, Hans-Jürgen, 540
Flavipinnis, 537
Forficula auricularia, 922
Forficula, 925, 927, 929
Fossil calibration, 269
Fossil record, 891
  relationship between cladistic/stratigraphic congruence and the completeness of, 899, 900
Fournier, E., see Aguileta, G., 613
Frutidella caesioatra, 143
Fugu, 421
Functional constraint, 591
Fundulus, 537
Fungi, 613
FUNYBASE, 613
Fusarium graminearum, 615
G. aculeatus, 521
G3pdh, 704
Gadus, 537
Gallotia-Galloti, 284
Gallus, 421
Gambusia, 537
Ganley, Austen R. D., see Regier, Jerome C., 920
Gap excess ratio, 891
GARLI program, 770
Gasterosteus, 537
Gastropoda, 514
Gatesy, John, see Deméré, Thomas A., 15
Gatesy, John, see McGowen, Michael R., 574
Gavialis gangeticus, 173
Gavialis, 178, 181
GBSSI, 704
Geisler, Jonathan H., see Asher, Robert J., 311
Gekko gecko, 421
GenBank
  data, 335
  taxonomic diversity, 336
  annotations, 336
  tracking changes, 342
  release 159, 342
Gendrault-Jacquemard, A., see Aguileta, G., 613
Gene content tree, 844
Gene Mapper, 358, 359
Gene trees, 243, 249, 420, 719
  congruence between, 723, 724
  statistical consistency of ML species supertrees for, 246, 247
  true, 247
  estimation of, 294, 295
  a posterior distribution of, 299
  probability density function of, 299
  topologies, 300
  versus concatenated tree versus species trees, 304–306
Gene-tree discordance, 876
Gene-tree reconciliation, 574
General no-common-mechanisms, 670
Genetic distance, 219
Genetic drift, 591
  rate of phenotypic evolution by, 594
  heterogeneous rate, 595, 597
  constant-rate, 596
  neutral, 600
Genista, 279, 748
Genome phylogeny, 844
Genome phylogeographic history, 559
Genomes, 855
Genomic Outposts Serve the Phylogenomic Pioneers: Designing Novel Nuclear Markers for Genomic DNA Extractions of Lepidoptera, Niklas Wahlberg and Christopher West Wheat, 231
Gentiana, 73
Geocarpa, 475
Geodesic distance, 436
Geomydoecus oregonus, 464
Geomys breviceps, 297
Gesneriaceae, 693
Ghosts of Gondwana, 329, 331
Ghosts of Gondwana: The History of Life in New Zealand, Michael D. Crisp, 329
GHR, 500
GI, 338
Giardia-Lamblia, 840
Gilia, 283
Ginnala, 800
Giraud, T., see Aguileta, G., 613
Gitzendanner, Matthew A., see Jian, Shuguang, 38
Glesne, 537
Glochidion, 463
Glomerata, 467

Glyceria striata, 485
Glycine, 480
Glyphopeltis ligustica, 143
Glyphorynchus spirurus, 729, 731
Glypta, 940
Glyptapanteles, 940
gncm, 670, 671, 673
Gnetum, 808
Gobipteryx, 192
Gorilla, 505
Grabaui, 188
Grande Coupure, 69, 74
Grantiopsis, 392
Grasses, 483
  clades of, 489
  cool season, 484, 489, 495
  endophyte-infected, 484
Greedy algorithm, 825
  for MAD, 832
GREEDYMMD, 827, 830, 831, 833
  HisA, 836, 838
Greta, 237
Grimm, Guido W., see Renner, Susanne S., 795
Growth heterochrony, 378
Gryllus firmus, 172
Gryposuchus, 180
GR, 575, 579, 580
GS, 478
Gsx, 708, 712, 714, 715
GTR, 206–211, 213
Gymnoderma, 156
Gymnotus, 172
Gyrodactylus, 463
H. annuus, 466
H. anomalus, 466
H. carolinensis, 391
H. deserticola, 466
H. desmarestianus, 465
H. irroratus, 465
H. muscivorus, 279, 280
H. mustelina, 259
H. paradoxus, 466
H. petiolaris, 466
H. pictus, 465
H. salvini, 465
Haasiophis terrasanctus, 322
Haasiophis, 322
Haematomma ochroleucum, 143
Hafner, Mark S., see Light, Jessica E., 449
Halecania alpivaga, 143, 144
Halecania, 153
Halictus, 889
Hallopus victor, 179
Handeliodendron bodinieri, 796
Handeliodendron, 796, 798
Hanseniella, 922
Haplotype trees, 639
Harbansus paucichelatus, 922
Hardman, Lotta M., see Hardman, Michael, 116
Hardman, Michael and Hardman, Lotta M., The Relative Importance of Body Size and Paleoclimatic Change as Explanatory Variables Influencing Lineage Diversification Rate: An Evolutionary Analysis of Bullhead Catfishes (Siluriformes: Ictaluridae), 116
Harmon, Luke J., Melville, Jane, Larson, Allan, and Losos, Jonathan B., The Role of Geography and Ecological Opportunity in the Diversification of Day Geckos (*Phelsuma*), 562
Harmon, Luke J., see Revell, Liam J., 591
Harrison, Luke B., and Larsson, Hans C. E., Estimating Evolution of Temporal Sequence Changes: A Practical Approach to Inferring Ancestral Developmental Sequences and Sequence Heterochrony, 378
Hassianycteris, 502
Hastings ratio, 86
Hawai'i, 4
Heath, Tracy A., Zwickl, Derrick J., Kim, Junhyong and Hillis, David M., Taxon Sampling Affects Inferences of Macroevolutionary Processes from Phylogenetic Trees, 160
Heathcote, Julia F., see Wills, Matthew A., 891
Heating parameter, 393
Helianthus deserticola, 480
Helianthus, 466, 481
Helichrysum frigidum, 280
Helichrysum, 283
Helicodiceros muscivorus, 269, 271, 272, 277, 279, 281–283
Helicodiceros, 271, 272, 276, 279, 280, 282
Heliconius melpomene, 232, 241
Heliconius, 233, 235, 237, 308, 730
Helobdella robusta, 711
Helobdella triserialis, 711
Helocarpon crassipes, 143
Helocarpon, 142, 153
Hemidactyliini, 514
Hemiplasy: A New Term in the Lexicon of Phylogenetics, John C. Avise and Terence J. Robinson, 503
Hendry, Tory A., see Jian, Shuguang, 38
Hepialus, 240
Herbert, Dai, Phylogeny and Evolution of the Mollusca, 955
Herbold, Craig W., see Lake, James A., 835
Herpetocetus, 31
Herteliana taylorii, 143
Hesionidae, 514
Hesperornis, 185, 187
Heterochone calyx, 389
Heterochone, 389, 391, 395, 396, 402
Heterochrony, 378
  on a single phylogeny, 379, 380
  debt, 385
Heteromys pictus, 451
Heteromys, 449, 453, 454, 456, 457, 465
Heteropodarke, 514
Heuchera, 56
Heuristics, 759
Hexasters, 400
Hexactinella carolinensis, 389
Hexactinella, 391, 395, 396, 398
Hexactinellida, 388
  taxonomy of, 394
  molecular phylogeny of, 396, 399
  phylogeny of, 400–402
Hexagenia limbata, 922
Hexapoda, 931
Hierarchical clustering, 104
Hierarchical likelihood-ratio test (hLRT), 76, 84
Hillebrandia sandwicensis, 327
Hillis, David M., see Heath, Tracy A., 160
Hines, Heather M., Historical Biogeography, Divergence Times, and Diversification Patterns of Bumble Bees (Hymenoptera: Apidae: *Bombus*), 58
Hiodon, 538
Hirudo medicinalis, 711
Historical Biogeography, Divergence Times, and Diversification Patterns of Bumble Bees (Hymenoptera: Apidae: *Bombus*), Heather M. Hines, 58

Historical biogeography, 4, 116, 257, 432
Quantitative statistical inference in, 4
methodological links between character evolution and, 11, 12
constraints on range evolution, 12
Historis, 237
HKY, 208, 212
HLRT, 76–79
Holarctic, 58
Holcus mollis, 485
Holder, Mark T., Sukumaran, Jeet and Lewis, Paul O., A Justification for Reporting the Majority-Rule Consensus Tree in Bayesian Phylogenetics, 814
Holland, Barbara R., Clarke, Andrew C., and Meudt, Heidi M., Optimizing Automated AFLP Scoring Parameters to Improve Phylogenetic Resolution, 347
Holostei, 519
Homeobox, 708
Homo sapiens, 20, 33, 469, 521, 574, 576, 583, 620, 780, 921, 926, 932
Homo, 174, 175, 341, 421, 505, 537, 922
Homoplasy, 503
Homoplasy, 251
Hoover, Paul, see Stamatakis, Alexandros, 758
Hoplodactylus maculatus, 285
Hordelymus europaeus, 485
Hordeum brevisubulatum, 485
Hordeum marinum, 283, 644
Host, 449
multi host parasite, 460
vertebrate, 460
switching, 462
parasite relationship, 462
Hox1, 708, 712, 714, 715
Hox10, 712
Hox14, 708
Hox2, 708, 712, 714, 715
Hox3, 708, 712, 714, 715
Hox4, 708, 712, 714, 715
Hox5, 712, 714, 715
Hox6, 714, 715
Hox7, 715
Hox8, 708, 714, 715
Hox9, 708, 712, 714, 715
Hoya, 482
Huelsenbeck, John P., Ané, Cécile, Larget, Bret, and Ronquist, Fredrik, A Bayesian Perspective on a Non-parsimonious Parsimony Model, 406
Huelsenbeck, John P., see Lakner, Clemens, 86
Huelsenbeck, John P., see Munch, Kasper, 750
Huson, Daniel H., see Whitfield, James B., 939
Hussey, April, see Regier, Jerome C., 920
Hutchinsoniella macracantha, 922
Hyalonema, 389, 391, 395, 396, 401
Hybridization, 466
versus the sorting of ancestral polymorphisms tested by coalescence simulation, 477–479
Hybridization, 876
Hydra circumcincta, 392
Hydra littoralis, 392
Hydra, 392
Hydrozoa, 392
Hylaeochampsa vectiana, 181
Hyliota, 267
Hylocichla, 259
Hypanartia, 235
Hypericum balearicum, 280
Hypericum, 282
Hyperoodon planifrons, 862
Hyperoodon rostratus, 30
Hypochaeris, 366
Hypochilus thorelli, 644
Hypochilus, 644
Hypogymnia physodes, 143
Hypothesis tests, 76
ML hypothesis test, 79
model-averaged, 81
outcome of, 83
Hypotheticus, 511
Hypotrigona, 60
Hypsipetes, 573
Högnabba 101, 143
I. australis, 117
I. balsanus, 117, 119
I. batatas, 351
I. dugesi, 116, 117, 119
I. furcatus, 117, 119
I. lupus, 119, 121, 125
I. meridionalis, 116, 117, 119
I. mexicanus, 117, 119
I. naevia, 259
I. ochoterenai, 116, 119
I. panicea, 396, 402
I. pricei, 117, 119
I. punctatus, 119, 121, 125–127
I. tiliacea, 351, 355
Iaceornis, 188
Iberomesornis, 188
Icaronycteris, 502
ICBN, 507–512
Ichthyornis, 185, 200, 514
ICPN, 507
Ictalurus furcatus, 118, 121, 122, 126, 127
Ictalurus lupus, 118
Ictalurus punctatus, 117–119, 791
Ictalurus rhaea, 119
Ictalurus, 116, 117, 119, 121, 125, 126, 538
ICZN, 507–513
Immigration-mutation-death process, 772
Importance sampling, 294
In silico, 365
Incertae sedis, 390, 391, 396, 402, 405
Incomplete lineage sorting, 202, 294
of daughter species, 295
demographic scenarios of, 305
Incomplete lineage sorting, 719
Incongruence length difference (ILD) test, 104
Incongruence, 466
test of, 472
various causes of, 474–477
among data sets, 479
Incongruence, 613
Indels, 835
Independent contrasts, 129
Indian Ocean, 562
Indopacetus pacificus, 873
Indostomus paradoxus, 315
Inferring Species Membership Using DNA Sequences with Back-Propagation Neural Networks, A. B. Zhang, D. S. Sikes, C. Muster, and S. Q. Li, 202
Inocybe, 155
Insecta, 752–755
Institutional abbreviations:, 34
Intercept, 763, 767

Intermediary species, 432
and betweenness measure, 436, 437
removal of, 438
clustering value of, 438
Internal nodes, 338
International Code of Botanical Nomenclature, 507
International Code of Phylogenetic Nomenclature, 507
International Code of Zoological Nomenclature, 507
Interpenetrate, 435
Intertextae, 474, 475, 481
Introgression, 876
Intron conservation, 772
inference based on, 779–781
phyla representatives used in, 780
parameter estimates for, 781
Iphiteon panicea, 394, 396, 399, 401
Iphiteon, 391, 395, 398, 401
Ipomoea batatas, 349, 350
Ipomoea, 351, 353–364
IRBP, 501
Isanacetus laticephalus, 34
Isanacetus, 23
Ischyrochampsa meridionalis, 180
Isisfordia duncani, 177
Isohypsibius elegans, 923
Ithomia, 232, 242
Ixoreus, 259
Janjucetus hunderi, 17, 23, 34
Janussen, Dorte, see Dohrmann, Martin, 388
Jian, Shuguang, Soltis, Pamela S., Gitzendanner, Matthew A., Moore, Michael J., Li, Ruiqi, Hendry, Tory A., Qiu, Yin-Long, Dhingra, Amit, Bell, Charles D. and Soltis, Douglas E., Resolving an Ancient, Rapid Radiation in Saxifragales, 38
Kalanchoe, 42
Kelneriapis, 60
Keratosperma allenbyense, 284
KH test, 450
Kim, Junhyong and Sanderson, Michael J., Penalized Likelihood Phylogenetic Inference: Bridging the Parsimony-Likelihood Gap, 665
Kim, Junhyong, see Heath, Tracy A., 160
Kimura two-parameter (K2P) model, 77, 78, 81, 84
King, Matthew G., see Clark, John R., 693
Kishino, Hirohisa, see Seo, Tae-Kun, 367
KITLG, 17–19, 34
Kluyveromyces lactis, 615
Koeleria cristata, 485
Koelreuteria, 796
Kogia breviceps, 33, 578
Kogia sima, 574, 583
Kogia, 23
Krog & Timdal MAU61/08, 143
Kuczynski, Caitlin A., see Wiens, John J., 420
L. atrosanguinea, 149
L. fuscoatra, 149
L. kurilensis, 214
L. silacea, 142
Labidesthes, 537
Lacantunia enigmatica, 128
Lachnum, 156
Lactuca, 748
Lake, James A., Servin, Jacqueline A., Herbold, Craig W. and Skophammer, Ryan G., Evidence for a New Root of the Tree of Life, 835
Lakner, Clemens, van der Mark, Paul, Huelsenbeck, John P., Larget, Bret and Ronquist, Fredrik, Efficiency of Markov Chain Monte Carlo Tree Proposals in Bayesian Phylogenetics, 86
LALBA, 577, 579, 588
Lama guanicoe, 33
Lamium purpureum, 158
Landscape, 544
Lanfear, Robert and Bromham, Lindell, Statistical Tests between Competing Hypotheses of Hox Cluster Evolution, 708
Lapparentophis defrennei, 320
Large data sets, 38
Larget, Bret, see Huelsenbeck, John P., 406
Larget, Bret, see Lakner, Clemens, 86
Larson, Allan, see Harmon, Luke J., 562
Larsson, Hans C. E., see Harrison, Luke B., 378
Lateral gene transfer (LGT), 104, 113
Lateral gene transfer, 104
Lateral genetic transfer (LGT), 844, 845, 847, 848, 849, 852
Lateral genetic transfer, 844
Laudakia caucasia, 572
Lavatera, 269, 748
Lawing, A. Michelle, Meik, Jesse M. and Schargel, Walter E., Coding Meristic Characters for Phylogenetic Analysis: A Comparison of Step-Matrix Gap-Weighting and Generalized Frequency Coding, 167
Lebrun, M.-H., see Aguileta, G., 613
Lecania atrynoides, 143
Lecanora intumescens, 143
Lecanora, 141, 143, 145, 146, 150–154, 156
Lecanorales, 141
Lecidea atrosanguinea, 143
Lecidea fuscoatra, 142, 143
Lecidea silacea, 143
Lecidea turgidula, 143, 149
Lecidea, 149, 153, 154
Lecidella meiococca, 143
Lecontei, 876–878, 880, 886, 888
Lecontei, 885
Lee, Christopher J., see Alekseyenko, Alexander V., 772
Lehtonen, Samuli, Phylogeny Estimation and Alignment via POY versus Clustal + PAUP*: A Response to Ogden and Rosenberg (2007), 653
Leidyosuchus canadensis, 181
Leidyosuchus, 181
Leigh, Jessica W., Susko, Edward, Baumgartner, Manuela and Roger, Andrew J., Testing Congruence in Phylogenomic Analysis, 104
Lemmon, Alan R., and Lemmon, Emily Moriarty, A Likelihood Framework for Estimating Phylogeographic History on a Continuous Landscape, 544
Lemmon, Emily Moriarty, see Lemmon, Alan R., 544
Leotia lubrica, 156
Lepas anserifera, 922
Lepidoptera, 231
Lepidothrix coronata, 730
Lepidothrix coronta, 729
Lepisosteidae, 531, 532
Lepisosteus, 116, 519, 520, 527, 532, 537
Lepraria bergensis, 143
Lepraria lobificans, 143
Lepraria, 150
Leptocarabus, 207, 210, 214, 215
Leptopogon, 267
Leptospirae, 474
Lethe, 240
Leucascus, 392
Leuckarti, 391
Leucophanella, 514
Leucopsacus, 391, 395
Lewis, Paul O., see Holder, Mark T., 814

Li, Chenhong, Lu, Guoqing, and Ortí, Guillermo, Optimal Data Partitioning and a Test Case for Ray-Finned Fishes (Actinopterygii) Based on Ten Nuclear Loci, 519
Li, Guoliang, Steel, Mike, and Zhang, Louxin, More Taxa Are Not Necessarily Better for the Reconstruction of Ancestral Character States, 647
Li, Ruiqi, see Jian, Shuguang, 38
Li, S. Q., see Zhang, A. B., 202
Li, Wai Lok Sibon, see Ross, Howard A., 216
Libinia emarginata, 922
Libythea, 237
Libytheana, 235
Lichanura, 429
Lichens, 141
Light, Jessica E., and Hafner, Mark S., Codivergence in Heteromyid Rodents (Rodentia: Heteromyidae) and Their Sucking Lice of the Genus *Fahrenholzia* (Phthiraptera: Anoplura), 449
Likelihood function, 675
Likelihood methods, 693
Likelihood ratio testing, 104
Likelihood-ratio test (LRT), 43, 76, 105, 367
Liliopsida, 752–755
Limenavis, 188
Limnadia lenticularis, 922
Limulus polyphemus, 922, 923
Limulus, 925, 927
Lindstrom, A., see Schardl, C. L., 483
Lineage sorting, 307
Lineage sorting, 131, 466, 876
Lineage-through-time (LTT), 58
Lingula anatina, 711
Linnen, Catherine R. and Farrell, Brian D., Comparison of Methods for Species-Tree Inference in the Sawfly Genus *Neodiprion* (Hymenoptera: Diprionidae), 876
Liomys, 449, 454, 465
Liotrigona, 60
Liotrigonopsis, 60
Liotyphlops, 428
Liquidambar, 43, 55, 56
Lissodelphis borealis, 33
Lithobius forficatus, 922
Lithobius, 925, 927
Lithornis, 192
Liu, Liang, see Belfiore, Natalia M., 294
Liu, Liang, see Brumfield, Robb T., 719
Llanocetus denticrenatus, 30
Llanocetus, 22, 31
Lobodon carcinophagus, 15
Lolium arundinaceum, 485
Lolium edwardii, 485
Lolium multiflorum, 485
Lolium perenne, 485
Lolium, 485
Long branch attraction, 38
Lopadium disciforme, 143
Lopadium, 153
Lophius, 538
Lophocalyx, 391, 395, 398, 402
Losos, Jonathan B., see Harmon, Luke J., 562
Lotus, 748
Low copy nuclear genes, 466
Loxocemus, 429
Loxothylacus texanus, 922
LR1+nt3, 929
LR1, 923, 925–929, 935, 937, 938
Lu, Guoqing, see Li, Chenhong, 519
Lucius, 537
Lum, David E., see Brumfield, Robb T., 719
Lupularia, 474
Lutjanus, 533, 538
Lycodes, 533, 538
Lycopersicon, 365
Lygodactylus, 564, 566
Lynceus, 922
Lysichiton, 283
M. rhodopea, 473
M. arabica, 467, 473
M. arborea, 467, 468, 475
M. astroides, 468
M. aurantiacus, 719–723, 725, 728
M. auranticaus, 727
M. bahamondi, 874
M. bidens, 864, 865
M. biflora, 468, 482
M. blancheana, 467
M. bowdoini, 864, 871
M. brachycarpa, 468
M. cancellata, 481
M. candei, 719–723, 725, 727–729
M. carlhubbsi, 864, 865, 871
M. carstiensis, 467
M. ciliaris, 467, 473
M. constricta, 467
M. coronata, 467, 479
M. crassipes, 468
M. cretacea, 468, 475
M. densirostris, 861, 864–866, 871
M. disciformis, 467, 479
M. doliata, 467
M. edgeworthii, 466, 467
M. europaeus, 32, 864, 865
M. europeaus, 871
M. falcata, 480
M. fischeriana, 468
M. ginkgodens, 864, 865, 868
M. granadensis, 467, 473
M. grayi, 864, 865
M. hectori, 864, 865, 871, 872
M. heyniana, 467, 479, 482
M. huberi, 468, 482
M. hybrida, 480, 481
M. intertexta, 467, 473
M. italica, 467, 482
M. laciniata, 467
M. lanigera, 467, 482
M. laxispira, 467, 482
M. layardii, 859, 864, 868, 871
M. lesinsii, 467, 475, 482
M. littoralis, 467, 481
M. lupulina, 467, 474, 479, 482
M. manacus, 719–723, 725, 727–729
M. marina, 467, 473
M. micrococca, 149
M. minima, 467, 479
M. mirus, 32, 864, 865, 871
M. monspeliaca, 468
M. murex, 467
M. muricolepsis, 467, 473
M. noeana, 467
M. novaeangliae, 25
M. orbicularis, 467, 482
M. perrini, 864, 865, 870–872

M. peruvianus, 859, 864, 865, 870, 872
M. phrygia, 468
M. pironae, 467
M. platicarpa, 482
M. platycarpa, 466, 467, 473, 481
M. plicata, 467, 482
M. polymorpha, 467
M. popovii, 467, 473
M. praecox, 467, 479
M. prasina, 149
M. prostrata, 467
M. radiata, 467, 482
M. ralloides, 259
M. rhodopea, 467, 481
M. rigidula, 467, 481
M. rotata, 467, 482
M. ruthenica, 467, 473
M. sativa, 466–471, 473, 478–481
M. sauvagei, 467
M. secundiflora, 467, 482
M. shepardii, 467, 482
M. soleirolii, 467, 482
M. stejnegeri, 864, 865, 871
M. suavagei, 482
M. suffruticosa, 467, 480, 481
M. tenoreana, 467, 474, 479, 482
M. tornata, 481
M. traversii, 859, 860, 871
M. truncatula, 466, 467, 469, 471–473, 479, 481, 482
M. turbinata, 467
M. v. milleri, 728
M. vitellinus, 719–722, 725, 727–729
M. vitellinus/M. manacus, 727
M13(−21), 922
M13, 922
M13REV, 922
Mabuya, 572
Macaronesia, 732
Machiloides banksi, 922
Macrantha, 806
Macrobiotus islandicus, 923
Macroevolution, 905
Macrolepidotus, 538
Macrothele calpeiana, 643
Maculata/clarkii, 552
Maf_order, 681
Magnaporthe grisea, 615
Mahogoni, 538
Malacosaccus coatsi, 398
Malacosaccus, 391, 395, 398, 402
Malacostraca, 931
Male holotype, 646
Male paratype, 646
Mammalodon colliveri, 17, 23, 34
Manacus manacus, 720
Manacus, 719–721, 723–725, 727–730
Manakin, 719
Mandibulata, 920
manE, 723
Mansion, Guilhem, Rosenbaum, Gideon, Schoenenberger, Nicola, Bacchetta, Gianluigi, Rosselló, Josep A., and Conti, Elena, Phylogenetic Analysis Informed by Geological History Supports Multiple, Sequential Invasions of the Mediterranean Basin by the Angiosperm Family Araceae, 269
manW, 723
Maoricicada, 480, 730
Markov chain Monte Carlo, 86, 406, 675
Marpesia, 235
Marthey, S., see Aguileta, G., 613
Martin, Jeremy E. and Benton, Michael J., Crown Clades in Vertebrate Nomenclature: Correcting the Definition of Crocodylia, 173
Martin, Joel W., see Regier, Jerome C., 920
Martini, 188
mask1, 923
mask2, 923, 926
Mastigoproctus giganteus, 923
Mastigoproctus, 925, 927
mat, 272, 274, 276, 283, 807
matK, 41, 43, 55, 470
matR, 39, 41, 43
Matthiola bolleana, 749
Mauicetus, 15
Maureira-Butler, Iván J., Pfeil, Bernard E., Muangprom, Amorntip, Osborn, Thomas C., and Doyle, Jeff J., The Reticulate History of *Medicago* (Fabaceae), 466
Maximum likelihood (ML) estimate, 249
Maximum likelihood (ML), 797
Maximum Likelihood Inference of Geographic Range Evolution by Dispersal, Local Extinction, and Cladogenesis, Richard H. Ree and Stephen A. Smith, 4
Maximum Likelihood Supertrees, Mike Steel and Allen Rodrigo, 243
Maximum likelihood, 76, 104, 243, 406, 544, 708, 758
  approach to supertree, 247
  framework, 246
  statistical consistency, 248
  of the no-common-mechanism model, 415
  use of, 408
  estimation of ?, 547
  compared with other data, 551
Maximum parsimony, 251
  tree, 253
  score, 253
Mayoa, 274
McGowen, Michael R., Clark, Clay, and Gatesy, John, The Vestigial Olfactory Receptor Subgenome of Odontocete Whales: Phylogenetic Congruence between Gene-Tree Reconciliation and Supermatrix Methods, 574
McGowen, Michael R., see Deméré, Thomas A., 15
MCMC approaches, 86, 118
MCMC model, 409
Meade, Andrew, see Venditti, Chris, 286
Median tree, 785
Medicago hypogaea, 475
Medicago lupulina, 479
Medicago rigiduloides, 481
Medicago ruthenica, 481
Medicago sativa, 480, 481
Medicago saxatilis, 481
Medicago sinkiae, 481
Medicago syriaca, 481
Medicago truncatula, 469, 480
Medicago, 466–471, 473–482
Medicago, 466
Mediterranean Basin, 269
Megachile rotundata, 479
Megalaria grossa, 143
Megalaria, 153
Megaptera hubachi, 34
Megaptera longimana, 33
Megaptera miocaena, 34
Megaptera novaeangliae, 23, 25, 33, 34, 872
Megaptera, 25, 32

Megascapheus, 295–298, 300, 302, 305–307
Meier, Rudolf, Zhang, Guanyang and Ali, Farhan, The Use of Mean Instead of Smallest Interspecific Distances Exaggerates the Size of the "Barcoding Gap" and Leads to Misidentification, 809
Meik, Jesse M., see Lawing, A. Michelle, 167
Melanitis, 237
Melanobombus, 68
Melanoplus, 365, 730, 889
Melanopus, 506
Melanorosaurus, 904
Melichthys niger, 906, 907, 916
Melichthys vidua, 907
Melichthys, 906, 910, 912, 916
Melilotus, 466
Melipona grandis, 60
Meliponula bocandei, 60
Melitaea cinxia, 232, 233
Melitaea, 237
Melville, Jane, see Harmon, Luke J., 562
Mendacibombus, 59, 69, 71
Menidia, 172
Meredith, Robert W., see Springer, Mark S., 499
Merlia normani, 405
Mertensiella luschani, 573
Mesocetus argillarius, 32
Mesocyclops edax, 922
Mesocyclops, 925, 927, 929, 935, 936
Mesoplodon bahamondi, 874
Mesoplodon bidens, 33, 34
Mesoplodon bowdoini, 872, 873
Mesoplodon carlhubbsi, 873
Mesoplodon densirostris, 30, 873
Mesoplodon gervaisi, 873
Mesoplodon grayi, 30, 858
Mesoplodon hectori, 873
Mesoplodon layardii, 874
Mesoplodon mirus, 873
Mesoplodon perrini, 873
Mesoplodon peruvianus, 33, 34
Mesoplodon traversii, 874
Mesoplodon, 22, 31, 32, 857–860, 862–868, 870–874
Metajapyx subterraneus, 922
Metazoan phylogeny, 388
Methanopyrus kandleri, 855
Methona, 235
Meudt, Heidi M., see Holland, Barbara R., 347
Micarea alabastrites, 143
Micarea erratica, 143, 146
Micarea intrusa, 146
Micarea micrococca, 143, 146
Micarea sylvicola, 143, 146, 149
Micarea, 143, 145, 146, 149–153
Microdipodops, 449
Micromysticetus rothauseni, 32
Micromysticetus, 15
Microplitis, 940
Microraptor zhaoianus, 200
Middleton, Kevin M., see Clarke, Julia A., 185
Migratorius, 263, 264
Milnesium tardigradum, 923
Mimulus, 696, 705
Minimize deep coalescences (MDC), 876, 877, 879, 880
Minimum extension, 256
Minuta, 391
Miriquidica garovaglii, 143
Mitsukurii, 391, 398
Mitsukurii/R. nodastrella, 398
Mixocetus elysius, 34
Mixocetus, 23
Mixture models, 286
ML bootstrap pseudoreplicates (MLBPs), 121
Model averaging, 905
Model comparison, 367, 388
  of codon and amino acid model, 368
  61-dimensional SK-P0 and amino acid model, 369
  of paired-sites models, 393, 394
  of single-gene analyses, 394
  Tree topologies and PPs, 394
Model of Diversity, 828, 829
Model organism, 338
Model selection, 76, 665
  standard, 83
  relationship between model-fit and, 84
Molecular clock, 905
Molecular dating, 58, 269
Molecular evolution, 286
Molecular phylogeny, 562
Molecular rates, 449
Molissima, 695
Mollissima, 695
Mollusca, 514
Monanthes, 744
Monodelphis brevicaudata, 317
Monodelphis domestica, 521
Monodelphis, 537
Monopterus, 538
Monosiga brevicollis, 390, 392
Montastraea franksi, 392
Monticola, 261
Moore, Michael J., see Jian, Shuguang, 38
Morawanocetus, 22
More Taxa Are Not Necessarily Better for the Reconstruction of Ancestral Character States, Guoliang Li, Mike Steel, and Louxin Zhang, 647
Moritz, Craig, see Belfiore, Natalia M., 294
Morone, 533, 538
Morphological and Molecular Evidence for a Stepwise Evolutionary Transition from Teeth to Baleen in Mysticete Whales, Thomas A. Deméré, Michael R. McGowen, Annalisa Berta, and John Gatesy, 15
Morphology and Placental Mammal Phylogeny, Mark S. Springer, Robert W. Meredith, Eduardo Eizirik, Emma Teeling, and William J. Murphy, 499
Morphology, Paleontology, and Placental Mammal Phylogeny, Robert J. Asher, Jonathan H. Geisler, and Marcelo R. Sánchez-Villagra, 311
Morphometrics, 316
Morrison, David A., Phylogenetic Trees Made Easy: A How-to Manual, third edition, 658
Morrison, David A., The Cambridge Companion to the Philosophy of Biology, 822
Mos, 320, 322
Mosaic evolution, 185
Mosaicism, Modules, and the Evolution of Birds: Results from a Bayesian Approach to the Study of Morphological Evolution Using Discrete Character Data, Julia A. Clarke and Kevin M. Middleton, 185
Motacilla, 268
MPELT, 815
MRCA, 498
Mse, 351, 734
MT-CO2, 577–579

MT-CYB, 577–579, 586
MtDNA, 38
Muangprom, Amorntip, see Maureira-Butler, Iván J., 466
Mugil, 538
Mulcahy, Daniel G., see Wiens, John J., 420
Multibarbata, 538
Multidivtime, 798, 800
Multidivtime, 798
Multigene phylogenies, 613
Multilocus Phylogenetics of a Rapid Radiation in the Genus *Thomomys* (Rodentia: Geomyidae), Natalia M. Belfiore, Liang Liu, and Craig Moritz, 294
Multilocus phylogeny, 294
Multiple Colonizations, In Situ Speciation, and Volcanism-Associated Stepping-Stone Dispersals Shaped the Phylogeography of the Macaronesian Red Fescues (*Festuca* L., Gramineae), Antonio Díaz-Pérez, Miguel Sequeira, Arnoldo Santos-Guerra, and Pilar Catalán, 732
Munch, Kasper, Boomsma, Wouter, Huelsenbeck, John P., Willerslev, Eske and Nielsen, Rasmus, Statistical Assignment of DNA Sequences Using Bayesian Phylogenetics, 750
Murex, 475
Murphy, William J., see Springer, Mark S., 499
Murugan, Sumathi, see Ross, Howard A., 216
Mus musculus, 20, 33, 469, 521, 574, 711
Mus, 537
Muscivorus, 279
Musculus, 537
Museum abbreviations, 260
Muster, C., see Zhang, A. B., 202
Myadestes, 259
Mycale fibrexilis, 392, 396
Mycoblastus sanguinarius, 143
Mygalomorphae, 628
Mykiss, 538
Myophonus, 261
Myosotis, 285
Myria:genes, 930, 934, 936
Myriapoda, 931
Myriapoda, 920
  nonavian, 900
Myriophyllum, 42
Myripristis, 537
Mystacina, 329
Mysticetes, 574
Mysticeti, 15
N. abbotii, 883, 886, 888
N. autumnalis, 878, 879
N. baileyi, 119
N. compar, 883, 888
N. crypticus, 117
N. cubensis, 878
N. dubiosus, 889
N. elegans, 119
N. eremita, 259
N. exilis, 125
N. fasciatus, 119
N. gladiator, 117, 119
N. gyrinus, 127
N. hildebrandi, 119
N. insignis, 127
N. insularis, 878
N. maurus, 886
N. merkeli maestrensis, 878
N. merkeli, 888
N. miurus, 127
N. nigroscutum, 883, 886, 888
N. pratti, 886
N. stanauli, 117, 119
N. stigmosus, 119, 127
N. taedae taedae, 878
N. taedae, 883
nad5, 41, 43
Naegleria gruberi, 108
Naegleria, 109
Nananthea perpusilla, 280
Nananthea, 281
Narceus americanus, 922
Narceus, 925, 927
Narcissus, 517
Naso, 918
National Evolutionary Synthesis Center (NESCent), 1
Natural History, 184
Nature, 179
Naufraga balearica, 283
Naufraga, 280
ND2, 564, 566
ndhB, 41
ndhF, 41, 55
NDNA, 466
Nearest-neighbor influences, 675
Nebalia hessleri, 922
Nebalia, 925, 927, 929, 935, 936
Nectarinia, 573
Negundo, 806
Nematostella vectensis, 708
Neobulgaria pura, 156
Neochlamisus, 889
Neodiprion abietis, 889
Neodiprion fulviceps, 890
Neodiprion nigroscutum, 889
Neodiprion pratti, 889, 890
Neodiprion rugifrons, 889
Neodiprion virginianus, 889
Neodiprion, 876–878, 880, 881, 885–890
Neogonodactylus oerstedii, 922
Neopsacas, 404
Neoscopelus, 538
Neotoma fuscipes, 645
Neotyphodium aotearoae, 485
Neotyphodium coenophialum, 485
Neotyphodium gansuense, 485
Neotyphodium lolii, 485
Neotyphodium occultans, 485
Neotyphodium typhinum, 485
Neotyphodium, 485
Nepeta cataria, 158
Nereis virens, 711
Nesocichla, 258, 259, 263
Neuquenornis, 192
Neural networks, 202
  memory of, 203
  output of, 203
  definition of, 203
Neurospora crassa, 613, 615
New Systematics, 661
Niche conservatism, 591
Niche-based distribution modeling, 628
Nicoletia meinerti, 922
Nielsen, Rasmus, see Munch, Kasper, 750
Nipponopsalis abei, 923
Nitophyllites zaisanicus, 276

Nodastrella, 391
Node clusters, 338
Node-density effect, 286
  magnitude of the reduction in, 289
  degree of, 287
Noguerornis, 188
noLR1+nt2, 923, 925–929, 931, 933, 935–938
noLR1, 923, 926, 927
noLR1nt2, 926
Noninformative ternary characters, 540
Nonparametric bootstrap, 76
Normania, 747
Norops auratus, 513
Norops, 513
North American ichthyofauna, 116
Notemigonus, 537
Nothofagus, 330, 331
Notocetus vanbenedeni, 32
Noturus albater, 118
Noturus baileyi, 118
Noturus crypticus, 119, 129
Noturus elegans, 118
Noturus eleutherus, 118, 127
Noturus exilis, 118, 125
Noturus fasciatus, 118
Noturus flavater, 118
Noturus flavipinnis, 118
Noturus flavus, 118, 127
Noturus funebris, 118
Noturus furiosus, 118
Noturus gilberti, 118
Noturus gladiator, 129
Noturus gyrinus, 118
Noturus hildebrandi, 118
Noturus insignis, 118
Noturus lachneri, 118
Noturus leptacanthus, 118
Noturus maydeni, 116, 118
Noturus miurus, 118
Noturus munitus, 118
Noturus nocturnus, 118
Noturus phaeus, 118
Noturus placidus, 118
Noturus stanauli, 129
Noturus stigmosus, 118
Noturus taylori, 118
Noturus, 116–119, 121, 125–129
Novaeangliae, 25
NRinter, 434
NRintra, 434
nt1, 923, 937
nt12 and nt3, 925
nt12, 923, 925, 927, 928, 930, 931, 935, 937, 938
nt123, 923, 925–929, 935
nt123-, 929
nt2, 923, 925–927
nt3, 923, 926–929, 935, 937
ntLR1+nt2, 928
Nuclear genes, 920
Nuclear introns, 857
  amplification of, 860, 862t
  analysis of, 871
  nuclear, 860
  observed level of, 894
Nuclear loci, 519
Nuclear ribosomal DNA, 38
Nuclear ribosomal RNA gene (nrLSU), 142, 144, 145, 147
Nucleotide composition, 927
Nudibranchia, 514
Nye, Tom M. W., , Trees of Trees: An Approach to Comparing Multiple Alternative Phylogenies, 785
Nylander, Johan A. A., Olsson, Urban, Alström, Per, and Sanmartín, Isabel, Accounting for Phylogenetic Uncertainty in Biogeography: A Bayesian Approach to Dispersal-Vicariance Analysis of the Thrushes (Aves: *Turdus*), 257
Nymphalidae, 231
Nymphalis, 242
O. glandulosa, 366
O. latipes, 521
O. macrophylla, 366
O. modesta, 366
O. moesta, 259
O. oenanthe, 259
O. pleschanka, 259
O. simpsonii, 366
OCP, 439, 441, 448
Odontocetes, 574
  database for, 575
  degradation of olfaction in, 580
Odontotrigona haematoptera, 60
Odonus niger, 907
Odonus, 906, 910, 912, 916
Oenanthe, 259, 261
Olea europaea, 746, 748
Olfactory receptors, 574
Oligobalistes robustus, 909
Oligobalistes, 906
Ollerton, Jeff, Ecology and Evolution of Flowers, 516
Olmstead, Richard G., see Cantino, Philip D., 157
Olsson, Urban, see Nylander, Johan A. A., 257
Ombrophila violacea, 156
On Evolution, Danny Yee, 184
On Growth and Form, 185
On the Distributions of Bootstrap Support and Posterior Distributions for a Star Tree, Edward Susko, 602
Oncorhynchus mykiss, 791
Oncorhynchus, 538
One-interval data set, 288
Onthophagus, 873
Oopsacas minuta, 390, 404
Oopsacas, 391, 395
Oopsacas/Leucopsacus, 396
Optimal Data Partitioning and a Test Case for Ray-Finned Fishes (Actinopterygii) Based on Ten Nuclear Loci, Chenhong Li, Guoqing Lu, and Guillermo Ortí, 519
Optimizing Automated AFLP Scoring Parameters to Improve Phylogenetic Resolution, Barbara R. Holland, Andrew C. Clarke, and Heidi M. Meudt, 347
OR10A1, 579
OR10AB1, 579, 583, 584
OR10AB2, 584
OR10J1, 579, 583, 588
OR10J2, 579, 583
OR10K1, 579
OR10K3, 579
OR13F1, 579, 583
OR13J1, 579, 580, 583, 586
OR13J1B, 579
OR1I1, 579, 580, 583, 584, 588
OR2AT1, 579
OR6M1, 579, 583, 584

Orchesella imitari, 922
Orcinus orca, 576–578, 583, 588
Oreochromis, 533, 538
Origin and Evolutionary Radiation of the Mollusca, 955
Origin of life, 840
Ornithorhynchus, 175
Orontium, 283
Orthogeomys grandis, 450
Orthogeomys heterodus, 297
Orthology, 503
Ortí, Guillermo, see Li, Chenhong, 519
Orycteropus afer, 316
Oryza sativa, 338
Oryzias, 533, 537
Osborn, Thomas C., see Maureira-Butler, Iván J., 466
Oscarella tuberculata, 392
Osteoglossum, 538
Ourisia crosbyi, 366
Ourisia, 350, 351, 353–366
Overall directionality test, 552
Ovis dalli, 33
Ovophis okinavensis, 431
p-Median, 832, 833
P. borbonica borbonica, 564
P. borbonica mater, 564
P. borbonica, 566
P. brachyphona, 549
P. brimleyi, 549
P. cepediana A, 564
P. comorensis, 566, 568
P. comoroensis, 571
P. crassidens, 588
P. edwardnewtonii, 571
P. feriarum, 549, 551, 552, 554–556
P. flavipes polionota, 259
P. flavus, 465
P. fouquettei, 549
P. fuscus, 909
P. g. rosagularis, 563
P. gigas, 571
P. guimbeaui guimbeaui, 563
P. hathewayi, 11
P. hawaiiensis, 8
P. kaduana, 8, 9, 11
P. kalmi, 549
P. leucops, 259
P. litsipsirupa, 259
P. longimembris, 465
P. m. kochi, 563
P. maculata, 549, 551, 556
P. maculata/clarkii, 549, 551
P. madagascarensis grandis, 563
P. mariniana, 8
P. mauiensis, 8
P. merriami, 465
P. nigrita, 549
P. o. inexpectata, 564
P. olivaris, 125, 127
P. ornata ornata, 564
P. parkeri, 564
P. pasteuri, 568
P. sundbergi longinsulae, 564
P. sundbergi sundbergi, 564
P. triseriata, 549, 556
P. v-nigra anjouanensis, 564
P. v-nigra comoraegrandensis, 564
P. v-nigra v-nigra, 564
Pachycladae, 748
Pachydactylus, 564, 566
Pachyspirae, 474, 475
Pacificus, 538
Paeonia, 39, 42, 46, 53, 284
Page, Roderic D. M. and Sullivan, Jack, The Expanding Contributions of ***Systematic Biology***, 1
Pagel, Mark, see Venditti, Chris, 286
Palaeochiropteryx, 502
Paleomap, 269
Pallimnarchus, 180
Palmata, 796, 800, 804, 806
Pan, 505
Pancrust:genes, 930, 934, 936
Pancrustacea, 931
Pancrustacea, 920
Papilio glaucus, 234
Papilio, 242
Papilionoideae, 344
Pappogeomys bulleri, 450
Parabalaenoptera baulinensis, 34
Paradoris dubia, 511
Paradoris, 511
Paradoxopoda, 920
ParaHox, 708
Paralamyctes grayi, 922
Paranephrops, 331
Paraphyletic, 640
Parapliosaccomys, 297
Pararge, 235
Parasite phylogeny mirrors host phylogeny, 462
Parasite, 449
  host and, 450, 451
  tree, 452, 453, 455
  COI gene, 453
  speciation, 462
  topologies, 462
  phylogenies, 454
Parastacoides, 331
Parasuchus, 177
Pareas, 430
Parent cluster, 338
Parent, 338
Parietobalaena palmeri, 32, 34
Parietobalaena, 23
Parmelia, 142
Parsimony length, 251
Parsimony model, 406
Parsimony via Consensus, Trevor C. Bruen and David Bryant, 251
Parsimony-based analyses, 39
Parsimony, 785
  bootstrapping in PAUP, 797
  with the Robinson-Foulds metric, 787
  meta-trees and, 787, 788
Passer, 174
Patagopteryx deferrariisi, 199
Pauropoda, 931
PCR, 231
PD, 831
Pectinopygus, 463
Pedetontus saltator, 922
Pedicularis, 73, 74
Pelagosaurus, 176
Pellona, 537
Pelocetus calvertensis, 34

Pelocetus, 23
Peltandra, 271, 277
Peltigera, 154
Penalized Likelihood Phylogenetic Inference: Bridging the Parsimony-Likelihood Gap, Junhyong Kim and Michael J. Sanderson, 665
Penalized likelihood, 665
  estimator for phylogeny, 666, 667
  maximum estimate of the tree, 668
  estimator, 670
  in tree inference, 671
Penthorum, 42
Per-generation, 546
Perfect phylogeny, 540
Perfectly Misleading Distances from Ternary Characters, Hans-Jürgen Bandelt and Mareike Fischer, 540
Pericallis, 748
Peridiscus, 43
Period, 242
Peripatric model, 595
Periplaneta americana, 922
Perognathus flavus, 452
Perognathus, 449, 453, 454, 456, 457, 459, 465
Peromyscus aztecus, 85, 536
Peromyscus maniculatus, 333
Pfeil, Bernard E., see Maureira-Butler, Iván J., 466
Phanerochaete chrysosporium, 615
Phascolion strombi, 711
Phelsuma andamanensis, 564
Phelsuma comorensis, 568
Phelsuma guentheri, 571
Phelsuma nigristrata, 568
Phelsuma robertmertensi, 568
Phelsuma, 562–567, 570–573
Pheronema carpenteri, 405
Pheronema, 391, 395, 396
Philippine endemic rodents, 292
Philoceanus, 464
Phocoena phocoena, 576, 578, 588
Phocoenoides dalli, 574, 583
Phryma, 705
Phylloscopus, 730
PhyloCode, 507–514
Phylogen, 162
Phylogenetic Analysis Informed by Geological History Supports Multiple, Sequential Invasions of the Mediterranean Basin by the Angiosperm Family Araceae, Guilhem Mansion, Gideon Rosenbaum, Nicola Schoenenberger, Gianluigi Bacchetta, Josep A. Rosselló, and Elena Conti, 269
Phylogenetic congruence, 104
Phylogenetic database, 335
Phylogenetic diversity, 825
Phylogenetic inference, 758
Phylogenetic informativeness, 613
Phylogenetic Mixture Models Can Reduce Node-Density Artifacts, Chris Venditti, Andrew Meade, and Mark Pagel, 286
Phylogenetic mixture models, 286
Phylogenetic nomenclature (PN), 173
Phylogenetic resolution, 347, 354, 355
Phylogenetic Signal, Evolutionary Process, and Rate, Liam J. Revell, Luke J. Harmon, and David C. Collar, 591
Phylogenetic supertree, 243
  estimates of, 243
  ML, 244
  triplet-based, 247
  likelihood-based, 247, 248
  subtree-to, 247
Phylogenetic Trees Made Easy: A How-to Manual, third edition, David A. Morrison, 658
Phylogenetic trees, 483
Phylogenetic variation, 419
Phylogenetically informative cluster, 338
Phylogenetics, 216, 378, 519, 591, 708, 750
  tree, 217, 220
  circumstances, 217
  scenario, 218
  software library of, 219
  model-based, 519
  risk of, 520
  pattern of relationships, 520
  topology, 378, 379, 381
  analysis in R, 383
  signal, 385
Phylogenomics, 104, 231, 335
  newly designed genes for, 233
  concept, 232
  goals of, 231
  analyses, 336
  GeneTrees, 339
Phylogeny and Evolution of Glass Sponges (Porifera, Hexactinellida), Martin Dohrmann, Dorte Janussen, Joachim Reitner, Allen G. Collins, and Gert Wörheide, 388
Phylogeny and Evolution of the Mollusca, 955
Phylogeny and Evolution of the Mollusca, Dai Herbert, 955
Phylogeny Estimation and Alignment via POY versus Clustal + PAUP*: A Response to Ogden and Rosenberg (2007), Samuli Lehtonen, 653
Phylogeny estimation, 665
Phylogeny inference, 85
Phylogeny of the Beaked Whale Genus *Mesoplodon* (Ziphiidae: Cetacea) Revealed by Nuclear Introns: Implications for the Evolution of Male Tusks, Merel L. Dalebout, Debbie Steel, and C. Scott Baker, 857
Phylogeny reconstruction, 286
  using Bayesian mixture, 288
  using Markov chains, 289
  making ancestral, 292
Phylogeny: phylogenomics, 420
  higher-level, 422
  methods, 428
  snake, 420, 421
  implication of, 429, 430
Phylogeny, 141, 347, 449, 574, 719, 857, 891
  of the order Lecanorales, 142
  Bayesian analyses of, 147
  53-taxon,
  and classification, 153, 154
  to changes in parameter settings, 359
  additional independent evidence for, 364
  simulated, 849
  multi-gene, 864
  p-median, 832, 833
  molecular, 870, 872
  robust, 859
Phylogeography, 544, 732
Phyloinformatics, 335
PhyloMapper, 544
PHYML(hrs)/GARLI(hrs), 767
Physeter macrocephalus, 30–34, 576, 578, 583
Physeter, 23, 586, 588
PI, 439, 440, 442, 444, 445, 448
Pieris rapae, 232, 233
Pinus, 478, 482
Pinusrigidae, 885

Pionopsitta, 731
Piscobalaena nana, 31
Pistia, 284
PKDREJ, 17–19, 34
PL, 666, 667, 670–672
Plakortis simplex, 392
Plasmodium, 108
Plastid inverted repeat, 38
Platanthera leucophaea, 748
Platanus, 39, 41
Platismatia glauca, 143
Platycichla, 258, 259
PLCB4, 500
Plebeia, 60
Plectrodon, 537
Plectroninia neocaledoniense, 392
Plethodon vandykei, 84
Plethodontidae, 514
Pleuronectes, 538
PLoS Biology, 1
PLoS One, 1
Pocket gopher, 294
Podarcis lilfordi, 284
Podarcis lilfordii, 279
Podarcis, 283
Podura aquatica, 922
Podura, 925, 927, 929
Poephila, 730
Pol II, 920–923, 926, 930, 931, 936, 937
Polychaeta, 514
Polygonia, 242
Polymerase chain reaction (PCR), 348
Polymixia, 533, 538
Polyodon, 116, 527, 537
Polypterus, 527, 532, 538
Polyxenus fasciculatus, 922
Porichthys, 537
Porifera, 388
Porphyra, 111
Porpidia, 889
Posterior probability, 602
  limiting distribution of, 603, 604
  limiting survivor function of, 608
Potamorhina laticeps, 442
Potamorhina latior, 443
Potamorhina pristigaster, 443
Potamorhina squamoralevis, 443
Potamorhina, 448
Potential, 344
Pratti, 880, 885, 886
Prietella, 117
Primers, 231
  cDNA-based, 232
  PCR, 232
  test, 233
Pristichampsus rollinatii, 180
PRM1, 17–19, 34, 577, 579
Probability, 131
  gene tree, 133
  general model, 131, 132
  overall, 132
  distribution, 132
Proctoporus, 172
Produces anomalies, 132
Progeomys, 297
Prokaryotes, 835
Proplebeia dominicana, 74
Proplebeia, 60
Proterochampsa, 179
Protoblastenia rupestris, 143
Protocalliphora, 214, 230
ProtoHox, 708
Protomicarea limosa, 143, 146
Protosuchus richardsoni, 176–178
Protosuchus, 179
Proxapertites, 285
psaI-accD, 704
psbA-trnH, 695–697, 699, 700, 796
psbB, 41
psbB-psbH, 704
psbB/T/N/H, 41
psbH, 41
psbM-trnD, 796
psbN, 41, 42
psbT, 41
Psectrogaster amazonica, 443
Psectrogaster essequibensis), 443
Psectrogaster falcata, 443
Psectrogaster rhomboides, 443
Psectrogaster rutiloides, 443
Psectrogaster saguiru, 443
Pseudacris brachyphona, 556, 560
Pseudacris feriarum, 544, 548–556, 558
Pseudacris kalmi, 549, 551
Pseudacris triseriata triseriata, 560
Pseudacris, 544, 548, 551, 560, 561
Pseudacris, 544
Pseudergolis, 235
Pseudobalistes flavimarginatus, 907, 910
Pseudobalistes fuscus), 910, 916
Pseudobalistes fuscus, 907, 909, 910, 916
Pseudobalistes viridescens, 916
Pseudobalistes, 905, 910, 912, 916
Pseudocurimata patiae, 442
Pseudocurimata, 442, 448
Pseudogenes, 574
  phylogenetic utility of, 574
  OR, 575
  and optimization of nonsense mutations, 576, 577
  Percentage of, 583
Pseudorca crassidens, 33, 576, 578, 588
Pseudoryx nghetinhensis, 31
Psilolechia leprosa, 143
Psilolechia lucida, 143
Psithyrus, 59, 62, 68–70, 73–75
Psittacula, 572
Psophocichla, 258, 259, 263
Psora decipiens, 143
Psora rubiformis, 143
Psora, 145, 146, 150–153
Psorula rufonigra, 143
Psorula, 145
Psychotria, 4, 6, 8, 9, 11–13, 704, 706
Psychotria, 4
Pteropus, 315
Pterostemon, 43
Puccinia graminis, 620
Purussaurus, 180, 181
Pycnogonida, 931
Pycnogonida, 920
Pygmaeus, 310
Pygocentrus, 537

Pylodictis olivaris, 117–119, 121, 126, 127
Pylodictis, 119, 121, 125–127
Pyrobombus, 62, 68–70, 74
Pyrococcus, 855
Pyron, R. Alexander, see Burbrink, Frank T. 317
Pyrrhospora quernea, 143
Qiu, Yin-Long, see Jian, Shuguang, 38
Quantitative characters, 591
Quartet puzzling, 771
Quercus, 795
Quinkana, 181
R. aculeatus, 912
R. assasi, 912
R. lunula, 910, 912
R. nodastrella, 398, 402
R. nuda, 398
R. pinicola, 259
R. racovitzae, 398
R. rectangulus, 910, 912
R. tintinnus, 391, 398
R. verrucosus, 910, 912
RA, 648, 649
Rabida, 125
Racovitzae, 391
Radiation of the Genus, 866
RAG, 501
rag1, 129
RAG1, 17–19, 34, 577, 579, 588
Rag2, 117, 118, 129
RAG2, 577
Rahonavis, 188
Ramalina fastigiata, 143
Ramalina, 142
Random exchanges, effects of directed versus, 854, 855
Random subtree pruning and regrafting (rSPR), 87, 89, 91
Random walk, 544
Randomization, 891
Ranidae, 327
Rapid bootstrap(RBS), 758
  heuristics in RAxML, 758, 759
  search, 760, 762
  Outline of, 761
Rapid radiation, 38
Rattus norvegicus, 20, 33, 469
RAxML program, 765
RAxML, 758
Ray-finned fish, 519
  diversity, 521
  characteristics of the ten nuclear loci amplified in, 523
  phylogenetic relationships among, 527
  Strict consensus tree of, 530
rbc, 56, 272, 274, 276, 807
rbcL, 41, 54–56, 160, 328, 410, 414, 796–798, 800, 801, 807, 808
RBS(Bips), 763, 765
RBS(hrs), 762
Real time, 925
Reconciled trees, 590
Ree, Richard H. and Smith, Stephen A., Maximum Likelihood Inference of Geographic Range Evolution by Dispersal, Local Extinction, and Cladogenesis, 4
Ree, Richard H., see Clark, John R., 693
Reeder, Tod W., see Wiens, John J., 420
Regalecus, 537
Regier, Jerome C., Shultz, Jeffrey W., Ganley, Austen R. D., Hussey, April, Shi, Diane, Ball, Bernard, Zwick, Andreas, Stajich, Jason E., Cummings, Michael P., Martin, Joel W. and Cunningham, Clifford W., Resolving Arthropod Phylogeny: Exploring Phylogenetic Signal within 41 kb of Protein-Coding Nuclear Gene Sequence, 920
Reitner, Joachim, see Dohrmann, Martin, 388
Relative proximity, 435
Relaxed clock, 116
  MCMC approach, 118
  UCLN modelling, 119
Relictus, 310
Renner, Susanne S., Grimm, Guido W., Schneeweiss, Gerald M., Stuessy, Tod F. and Ricklefs, Robert E., Rooting and Dating Maples (*Acer*) with an Uncorrelated-Rates Molecular Clock: Implications for North American/Asian Disjunctions, 795
Resolving an Ancient, Rapid Radiation in Saxifragales, Shuguang Jian, Pamela S. Soltis, Matthew A. Gitzendanner, Michael J. Moore, Ruiqi Li, Tory A. Hendry, Yin-Long Qiu, Amit Dhingra, Charles D. Bell, and Douglas E. Soltis, 38
Resolving Arthropod Phylogeny: Exploring Phylogenetic Signal within 41 kb of Protein-Coding Nuclear Gene Sequence, Jerome C. Regier, Jeffrey W. Shultz, Austen R. D. Ganley, April Hussey, Diane Shi, Bernard Ball, Andreas Zwick, Jason E. Stajich, Michael P. Cummings, Joel W. Martin, and Clifford W. Cunningham, 920
Retrotransposon, 499
Revell, Liam J., Harmon, Luke J., and Collar, David C., Phylogenetic Signal, Evolutionary Process, and Rate, 591
RF, 763, 764
RF-SBS/RF-RBS, 767
Rhabdocalyptus dawsoni, 404
Rhabdopectella tintinnus, 389, 398
Rhabdopectella, 391, 395, 398, 402
Rhinecanthus aculeatus, 907
Rhinecanthus assassi, 907
Rhinecanthus lunula, 907
Rhinecanthus rectangulus, 907
Rhinecanthus verrucosus, 907, 912
Rhinecanthus, 906, 910–912, 916
Rhinecantus, 906
Rhinotus purpureus, 922
Rhizocarpon, 154
Rhizopus oryzae, 615, 616
RHO, 874
Rhododendron, 73
Rhoptropella ocellata, 564, 566
Rhoptropus boultoni, 564
Rhoptropus, 573
Rhymphoctona, 947
Ribosomal DNA, 388
Richii, 695
Richtersius coronifer, 923
Ricklefs, Robert E., see Renner, Susanne S., 795
Ridgwayia, 259
Ripplinger, Jennifer and Sullivan, Jack, Does Choice in Model Selection Affect Maximum Likelihood Analysis?, 76
RLH(hrs), 766
RLH, 766
RNA secondary structure, 388
Roalson, Eric H., see Clark, John R., 693
Robinson, Terence J., see Avise, John C., 503
Robustus, 25
Rodolphe, F., see Aguileta, G., 613
Rodrigo, Allen G., see Bordewich, Magnus, 825
Rodrigo, Allen, see Steel, Mike, 243
Roger, Andrew J., see Leigh, Jessica W., 104
Rolfidium coccocarpioides, 143
Ronquist, Fredrik, see Huelsenbeck, John P., 406

Ronquist, Fredrik, see Lakner, Clemens, 86
Rooted, 251
Rooting and Dating Maples (*Acer*) with an Uncorrelated-Rates Molecular Clock: Implications for North American/Asian Disjunctions, Susanne S. Renner, Guido W. Grimm, Gerald M. Schneeweiss, Tod F. Stuessy, and Robert E. Ricklefs, 795
Rooting of phylogenies, 795
Root, 835
Rosellinia, 155
Rosenbaum, Gideon, see Mansion, Guilhem, 269
Rosenberg, Noah A. and Tao, Randa, Discordance of Species Trees with Their Most Likely Gene Trees: The Case of Five Taxa, 131
Ross, Howard A., Murugan, Sumathi, and Li, Wai Lok Sibon, Testing the Reliability of Genetic Methods of Species Identification via Simulation, 216
Rossella nodastrella, 402, 405
Rossella, 391, 395, 398, 402
Rosselló, Josep A., see Mansion, Guilhem, 269
Rotatae, 474, 475
Rougemont, Jacques, see Stamatakis, Alexandros, 758
Rozeni, 60
rp, 466, 469, 470, 472, 473
rpl16, 796
rpl2, 41
rpl23, 41
rpoC1, 480
rpoC2, 41–43
rps, 272, 274, 276, 284
rps12, 41
rps16, 87
rps3, 41, 43
rps4, 41–43
rps4-cob, 471
rps4/trnV, 41
rps7, 41
rrn16, 41
rrn23, 41
rrn4.5, 41
rrn5, 41
Rubra, 804, 806
Rubra-Hyptiocarpa, 804
Rubus, 73
S. albicaudatum, 912
S. bayanus, 790, 791
S. bolanderi, 158
S. bredanensis, 588
S. bursa, 912
S. castellii, 790, 791
S. cerevisiae, 623, 790
S. chrysopterum, 912
S. coeruleoalba, 580
S. galericulata, 158
S. granosus, 445
S. kluyveri, 790, 791
S. kudriavzevii, 790, 791
S. lidii, 749
S. marshalli, 444, 445
S. mikatae, 790
S. nodorum, 618, 624, 625
S. paradoxus, 790
S. pombe, 623
S. pullus, 444, 445
S. sialis, 259
S. str., 400
S. thompsoni, 445
S. vulgaris, 259
Saccharomyces bayanus, 615
Saccharomyces castellii, 615
Saccharomyces cerevisiae, 613, 615, 621
Saccharomyces kluyveri, 615
Saccharomyces kudriavzevi, 615
Saccharomyces mikatae, 615
Saccharomyces paradoxus, 615
Saghatherium antiquum, 315
Sanderson, Michael J., Boss, Darren, Chen, Duhong, Cranston, Karen A., and Wehe, Andre, The PhyLoTA Browser: Processing GenBank for Molecular Phylogenetics Research, 335
Sanderson, Michael J., see Kim, Junhyong, 665
Sandiegensis, 513
Sanmartín, Isabel, see Nylander, Johan A. A., 257
Santalum, 702, 706
Santini, Francesco, see Dornburg, Alex, 905
Santos, Daniel A. Dos, Fernández, Hugo R., Cuezzo, María Gabriela, and Domínguez, Eduardo, Sympatry Inference and Network Analysis in Biogeography, 432
Santos-Guerra, Arnoldo, see Díaz-Pérez, Antonio, 732
Sapeornis, 188
Sarcosuchus imperator, 176
Sarcosuchus, 179
Sarga, 514
Satan eurystomus, 117
Sauromatum guttatum, 279
Sauromatum, 272, 276
Saxifraga flagellaris, 57
Saxifraga integrifolia, 43
Saxifraga, 749
Saxifragales, 38
SBS(Bips), 763, 765
SBS(hrs), 762
Sceloporus undulatus, 463
Sceloporus, 645
Schadonia fecunda, 143, 146
Schardl, C. L., Craven, K. D., Speakman, S., Stromberg, A., Lindstrom, A., and Yoshida, R., A Novel Test for Host-Symbiont Codivergence Indicates Ancient Origin of Fungal Endophytes in Grasses, 483
Schargel, Walter E., see Lawing, A. Michelle, 167
Schilbeodes, 125
Schismatoglottis, 282
Schizosaccharomyces pombe, 615
Schmidly, David J., Terry Lamon Yates, 333
Schneeweiss, Gerald M., see Renner, Susanne S., 795
Schoenenberger, Nicola, see Mansion, Guilhem, 269
Sciobius, 443–446, 448
Scleromochlus taylori, 178
Sclerotinia sclerotiorum, 615
Scoliciosporum intrusum, 143
Scoliciosporum umbrinum, 143
Scolopendra polymorpha, 922
Scoring parameters, 347
  automated, 364
  of AFLP, 364
Scutellaria bolanderi, 158
Scutellaria galericulata, 158
Scutellaria, 73, 158
Scutigerella, 922
Scyphozoa, 392
Sebastes, 538
Securidaca, 808
Selecting Taxa to Save or Sequence: Desirable Criteria and a Greedy Solution, Magnus Bordewich, Allen G. Rodrigo, and Charles Semple, 825

Semi-parametric, 665
Semibalanus balanoides, 922
Semotilus atromaculatus, 791
Semotilus, 537
Semperella schulzei, 396
Semperella, 391, 395
Semple, Charles, see Bordewich, Magnus, 825
Senecio jacobaea, 365
Senecio, 282
Seo, Tae-Kun, and Kishino, Hirohisa, Synonymous Substitutions Substantially Improve Evolutionary Inference from Highly Diverged Proteins, 367
Separate analysis, 104
  advantage of, 105
  lowers bootstrap support, 111
Sequeira, Miguel, see Díaz-Pérez, Antonio, 732
Sequence heterochrony, 378
Sequence heterochrony, 378
  identification of, 379, 380
  hypothetical, 380
Sequencing protocol, 907
Sericolophus hawaiicus, 396
Sericolophus, 391, 395
Serjania, 796
Sertifer, 877–879, 890
Servin, Jacqueline A., see Lake, James A., 835
Sexual selection, 857
SF(hrs), 766
Shallowest divergences (SD), 876
Shi, Diane, see Regier, Jerome C., 920
Shultz, Jeffrey W., see Regier, Jerome C., 920
Sialia, 259
Sikes, D. S., see Zhang, A. B., 202
Simulation, 286
Site-specific rates, 670
Sites Jr., Jack W., see Wiens, John J., 420
Skogsbergia lerneri, 922
Skophammer, Ryan G., see Lake, James A., 835
SLH, 766
Slowly evolving genes, 38
Smith, Sarah A., see Wiens, John J., 420
Smith, Stephen A., see Ree, Richard H., 4
Smith, Vincent S., The New Taxonomy, 660
Smithi, 263
Smyrna, 240
Solanum vespertilio, 749
Solanum, 365
Soleneiscus stolonifer, 392
Soltis, Douglas E., see Jian, Shuguang, 38
Soltis, Pamela S., see Jian, Shuguang, 38
Sonchus gandogeri, 748
Sonchus, 734, 744, 748
Songlingornis linghensis, 188
Songlingornis, 188, 189, 192, 193
Sorghum, 514
Sotalia, 589
Spatial expression, 439
Speakman, S., see Schardl, C. L., 483
Speciation in Birds, 515
Speciation in Birds, Glenn-Peter Sætre, 515
Speciation rate of evolution, 562
Speciation, 4, 116
Species choice, 833
Species delineation, 628
Species identification, 202
  success rate of, 207
  BP-based, 208, 209
Species identification, 216
  testing methods of
  discussion, 222, 226
  paraphyly and, 228
Species Names in the *PhyloCode*: The Approach Adopted by the International Society for Phylogenetic Nomenclature, Benoît Dayrat, Philip D. Cantino, Julia A. Clarke, and Kevin de Queiroz, 507
Species tree, 243, 294
  gene trees versus concatenated tree versus, 304, 306
  species tree analysis, 300
  distribution of, 299
Species tree, 719
  Bayesian estimation of, 724
  congruence between gene trees and, 725
  reconstruction, 725
  phylogenetic methods, 729
SpeedupF, 766
Speleonectes tulumensis, 922
Speleonectes, 925, 927, 929
Sphaerophorus globosus, 143
Sphaerophorus, 142, 150
Sphenodon guntheri, 330
Sphenodon, 175, 331
Sphenopholis obtusata, 485
Sphenosuchus acutus, 179
Spiders, 628
Spirocarpos, 474, 481
Split, 785
  definition, 787
  consensus of sets of, 788
  tree-like sets of, 789
Spongilla lacustris, 392, 396
SPR distance, 251
SPR distance, 251
SPR median tree, 253
SPR, 250
Springer, Mark S., Meredith, Robert W., Eizirik, Eduardo, Teeling, Emma, and Murphy, William J., Morphology and Placental Mammal Phylogeny, 499
SPTBN1, 577, 579
Squalodon calvertensis, 34
Squamarina lentigera, 143
Squamarina scopulorum, 154
SRY, 577
Stagonolepis Robertsoni, 179
Stagonolepis, 177
Stagonospora nodorum, 615, 616
Stajich, Jason E., see Regier, Jerome C., 920
Stamatakis, Alexandros, Hoover, Paul and Rougemont, Jacques, A Rapid Bootstrap Algorithm for the RAxML Web Servers, 758
Star tree, 602
  paradox, 602, 607
  simulation, 605
Starting tree, 578
STAT5A, 17–19, 34
Statistical Assignment of DNA Sequences Using Bayesian Phylogenetics, Kasper Munch, Wouter Boomsma, John P. Huelsenbeck, Eske Willerslev, and Rasmus Nielsen, 750
Statistical consistency, 243
  of ML supertree, 245, 247
  of MRP, 246
  for maximum likelihood, 248
Statistical phylogeography, 544
  primary aim of, 544
  coalescent-based approaches in, 556

to test for simultaneous vicariance in, 558
future of, 559, 560
Statistical Tests between Competing Hypotheses of Hox Cluster Evolution, Robert Lanfear and Lindell Bromham, 708
Statistically consistent, 249
Steel, Debbie, see Dalebout, Merel L., 857
Steel, Mike A., see Whitfield, James B., 939
Steel, Mike, and Rodrigo, Allen, Maximum Likelihood Supertrees, 243
Steel, Mike, see Li, Guoliang, 628
Steindachnerina argentea, 443
Steindachnerina atratoensis, 442
Steindachnerina biornata, 443
Steindachnerina brevipinna, 443
Steindachnerina conspersa, 443
Steindachnerina dobula, 443
Steindachnerina elegans, 442, 443
Steindachnerina fasciata, 443
Steindachnerina hypostoma, 443
Steindachnerina insculpta, 443
Steindachnerina leucisca, 443
Steindachnerina notonota, 443
Steindachnerina pupula, 443
Steindachnerina quasimodoi, 443
Steindachnerina runa, 443
Steindachnerina, 448
Stenella coeruleoalba, 580
Stenella coeruleoalba, 574, 576, 578, 579, 583, 586, 588
Steneosaurus, 175
Steno bredanensis, 576, 578, 588
Steno, 588, 589
Stereocaulon pileatum, 143
Stereocaulon tomentosum, 143
Stochastic Dollo, 772
multi-state model, 776, 778
binary model, 773–775
Stochastic mapping (SIMMAP), 141
Stochastic mapping, dispersal, 693
Stochastic nearest neighbor interchange (stNNI), 87
Stockman, Amy K., see Bond, Jason E., 628
Stomias, 538
Storeria dekayi, 379
Stratigraphic congruence, 891
choose between trees for the same taxa, 901, 902
and the completeness of the fossil record, 899, 900
existing indices of, 894
for dinosaurs, 902
Stratigraphic fit, 903
Streptocephalus seali, 922
Stricto, 388
Strobus, 482
Stromberg, A., see Schardl, C. L., 483
Strong, 929
Structure, 748
Struthio, 174
Stuessy, Tod F., see Renner, Susanne S., 795
Sturnus, 259, 261
Suberites ficus, 392, 396
Substitution rates, 539
Substitution rates, 795
Subterraneobombus, 68
Subtree clusters, 338
Subtree, 338, 344
Subtree-prune and regraft, 251
Suchard, Marc A., see Alekseyenko, Alexander V., 772
Sufflamen albicaudatum, 907
Sufflamen bursa, 907
Sufflamen chrysopterum, 907
Sufflamen fraenatum, 907, 911
Sufflamen, 906, 910–912, 916
Sukumaran, Jeet, see Holder, Mark T., 814
Sulfolobus, 844, 854
Sullivan, Jack, see Page, Roderic D. M., 1
Sullivan, Jack, see Ripplinger, Jennifer, 76
Sump, 234, 631
Sumt, 631
Superkingdom, 104
Supermatrix analysis, 104
Supermatrix, 574
and GR analyses, 575, 588
advantages of, 575
combined, 579
of OR genes and independent DNA data, 584
Supernetworks, 939
Supertree construction, 248
Supertree methods, 940
Supertree, 243
Supertrees, 243
Support values, 758
Sus scrofa, 26, 33
Susko, Edward, see Leigh, Jessica W., 104
Susko, Edward, On the Distributions of Bootstrap Support and Posterior Distributions for a Star Tree, 602
Svennblad, Bodil, Consistent Estimation of Divergence Times in Phylogenetic Trees with Local Molecular Clocks, 947
Symbiobacterium thermophilum, 840
Symbiosis, 449
Sympatry Inference and Network Analysis in Biogeography, Daniel A. Dos Santos, Hugo R. Fernández, María Gabriela Cuezzo, and Eduardo Domínguez, 432
Symphyla, 931
Symplocarpus, 283
Synapomorphy, 503
Synodus, 537
Synonymous saturation, 367
and Evolutionary Distance, 370, 371
effect of ignoring, 371
Synonymous Substitutions Substantially Improve Evolutionary Inference from Highly Diverged Proteins, Tae-Kun Seo and Hirohisa Kishino, 367
Systematic Biology, 1, 2, 43, 335, 440, 512, 822, 872, A-1
Syzygium, 403
Sánchez-Villagra, Marcelo R., see Asher, Robert J., 311
Sætre, Glenn-Peter, Speciation in Birds, 515
T. albicollis paraguayensis, 259
T. albicollis, 264
T. albocinctus, 259
T. amaurochalinus, 259
T. ambiguum, 468
T. anguina, 468
T. arabica, 468
T. assimilis dague, 259
T. aurantius, 259
T. b. awahnee, 305
T. balansae, 468
T. bewsheri, 259
T. bottae awahnee, 297, 300
T. bottae, 295, 297–300, 302, 304–307
T. boulboul, 259
T. bulbivorus, 295, 297, 300, 302, 304
T. caerulea, 468
T. calliceras, 468
T. cardis, 259, 265

T. celaenops, 259
T. chiguanco chiguanco, 259
T. chiguanco, 264
T. chrysolaus, 259
T. clusius, 295, 297, 306
T. corniculata, 468
T. cretica, 468
T. dissimilis, 259
T. falcklandii magellanicus, 259
T. feae, 265
T. foenum-graecum, 468
T. fulviventris, 259, 264
T. fumigatus, 259
T. fuscater fuscater, 259
T. fuscater, 264
T. glabra, 468
T. grayi, 259, 261
T. haplochrous, 259
T. hauxwelli, 259
T. hortulorum, 259
T. idahoensis, 295, 297, 300, 302, 306
T. ignobilis debilis, 259
T. iliacus iliacus, 259
T. iliacus, 264
T. infuscatus, 259
T. jamaicensis, 259
T. kessleri, 259
T. lawrencii, 259
T. leucomelas leucomelas, 259
T. libonyanus peripheris, 259
T. m. merula/T. m. intermedius, 264
T. macrorrhyncа, 468
T. maculirostris, 259
T. maranonicus, 259
T. maritima, 855
T. mazama, 295, 297, 300
T. merula intermedius, 260
T. merula mandarinus, 259
T. merula maximus, 260
T. merula merula, 260
T. merula simillimus, 260
T. mesopotamica, 468
T. migratorius migratorius, 260
T. migratorius, 266
T. monticola, 295, 297, 300, 302
T. mupinensis, 260, 261
T. naumanni eunomus, 260
T. naumanni naumanni, 260
T. nigrescens, 260
T. nigriceps, 260
T. nudigenis, 260
T. obscurus, 260
T. obsoletus parambanus, 260
T. olivaceousfuscus, 263, 265
T. olivaceuofuscus, 260
T. olivaceus abyssinicus, 260
T. olivaceus helleri, 260
T. olivaceus ludoviciae, 260
T. olivaceus nyikae, 260
T. olivaceus olivaceus, 260
T. olivaceus roehli, 260
T. olivaceus smithi, 260
T. olivater, 260
T. pallidus, 260
T. pelios centralis, 260
T. pelios saturatus, 260
T. pelios, 260, 263, 265
T. philomelos philomelos, 260
T. philomelos, 261
T. pilaris, 260, 264
T. plebejus, 260
T. plumbeus ardosiaceus, 260
T. plumbeus plumbeus, 260
T. poliocephalus hygroscopus, 260
T. poliocephalus kulambangrae, 260
T. poliocephalus niveiceps, 260
T. poliocephalus poliocephalus, 260
T. poliocephalus rennellianus, 260
T. poliocephalus thomassoni, 260
T. pratenses, 468
T. r. atrogularis, 266
T. r. ruficollis, 266
T. reevei, 260
T. rubripes, 521
T. rubrocanus gouldi, 260
T. rubrocanus rubrocanus, 260
T. ruficollis atrogularis (AB)–T. ruficollis ruficollis (B), 266
T. ruficollis atrogularis, 260
T. ruficollis ruficollis, 260
T. rufitorques, 260, 264
T. rufiventris, 260, 264
T. rufopalliatus, 258
T. serranus serranus, 260
T. serranus, 264
T. spicata, 468
T. spruneriana, 468
T. stellata, 468
T. suavissima, 468
T. swalesi swalesi, 260
T. talpoides, 295, 297, 300, 302, 306
T. tephronotus, 260, 263
T. torqatus torqatus, 260
T. torquatus–T. ruficollis, 265
T. townsendii, 295, 297, 300, 302, 304
T. tubulosum, 391
T. umbrinus, 295, 297, 302, 307
T. unicolor, 260, 265
T. viscivorus viscivorus, 260
Tachyglossus, 175
Takifugu, 538
Talpa europaea, 314, 315
Tamias amoenus, 84
Tamura-Nei model, 678
Tanystylum orbiculare, 923
Tanystylum, 925, 927, 929
Tao, Randa, see Rosenberg, Noah A., 131
Tapirus indicus, 33
Taq, 17, 469, 576
Tarsius bancanus, 316
Tasmacetus sheperdi, 22
Tasmacetus shepherdi, 34, 860, 874
Taxon ID, 338
Taxon names, 336
Taxon Sampling Affects Inferences of Macroevolutionary Processes from Phylogenetic Trees, Tracy A. Heath, Derrick J. Zwickl, Junhyong Kim, and David M. Hillis, 160
Taxon selection, 835
Taxon Selection, 835
Taxonomic distinctness (TD), 831, 832
  taxonomic distinctness, 831, 832
Taxonomic distinctness, 831
Taxonomy tree, 335

Taxus mairei, 681
Tayassu tajacu, 33
TBR, 250
TBX4, 577
Teeling, Emma, see Springer, Mark S., 499
Teeth, 857
  medial, 906, 916
  tusk-like, 857
  strap-like, 868
tefA, 489
Tegeticula yuccasella, 84
Tektin, 242
Teleosaurus, 175
Teline, 748
Teloschistes, 154
Temporal diversification, 905
Tenrecs, 316
Tenuis, 391, 398
Tephromela atra, 143
Terraenovae, 538
Terry Lamon Yates, David J. Schmidly, 333
Testing Congruence in Phylogenomic Analysis, Jessica W. Leigh, Edward Susko, Manuela Baumgartner, and Andrew J. Roger, 104
Testing the Reliability of Genetic Methods of Species Identification via Simulation, Howard A. Ross, Sumathi Murugan, and Wai Lok Sibon Li, 216
Tetracarpaea, 43
Tetragnatha, 562
Tetragonisca angustula, 60
Tetragonula fuscobalteata, 60
Tetramorium, 645
Tetraodon, 538
Tetraodontiformes, 905
Tetrapoda, 175
Texasophis galbreathi, 322
Thaleichthys, 538
Thamnophilus, 267
Thamnophis, 29
The Cambridge Companion to the Philosophy of Biology, David A. Morrison, 822
The Expanding Contributions of ***Systematic Biology***, Roderic D. M. Page and Jack Sullivan, 1
The Florida Naturalist, 184
The Impact of Reticulate Evolution on Genome Phylogeny, Robert G. Beiko, W. Ford Doolittle, and Robert L. Charlebois, 844
The Influence of Model Averaging on Clade Posteriors: An Example Using the Triggerfishes (Family Balistidae), Alex Dornburg, Francesco Santini, and Michael E. Alfaro, 905
The Limitations of Ancestral State Reconstruction and the Evolution of the Ascus in the Lecanorales (Lichenized Ascomycota), Stefan Ekman, Heidi L. Andersen and Mats Wedin, 141
The Modified Gap Excess Ratio (GER*) and the Stratigraphic Congruence of Dinosaur Phylogenies, Matthew A. Wills, Paul M. Barrett, and Julia F. Heathcote, 891
The New Systematics, 661
The New Taxonomy, 660, 662, 663
The New Taxonomy, Vincent S. Smith, 660
The PhyLoTA Browser: Processing GenBank for Molecular Phylogenetics Research, Michael J. Sanderson, Darren Boss, Duhong Chen, Karen A. Cranston, and Andre Wehe, 335
The Relative Importance of Body Size and Paleoclimatic Change as Explanatory Variables Influencing Lineage Diversification Rate: An Evolutionary Analysis of Bullhead Catfishes (Siluriformes: Ictaluridae), Michael Hardman and Lotta M. Hardman, 116
The Reticulate History of *Medicago* (Fabaceae), Iván J. Maureira-Butler, Bernard E. Pfeil, Amorntip Muangprom, Thomas C. Osborn, and Jeff J. Doyle, 466
The Role of Geography and Ecological Opportunity in the Diversification of Day Geckos (*Phelsuma*), Luke J. Harmon, Jane Melville, Allan Larson, and Jonathan B. Losos, 562
The Taming of the Skew: Estimating Proper Confidence Intervals for Divergence Dates, Frank T. Burbrink and R. Alexander Pyron, 317
The Use of Mean Instead of Smallest Interspecific Distances Exaggerates the Size of the "Barcoding Gap" and Leads to Misidentification, Rudolf Meier, Guanyang Zhang, and Farhan Ali, 809
The Vestigial Olfactory Receptor Subgenome of Odontocete Whales: Phylogenetic Congruence between Gene-Tree Reconciliation and Supermatrix Methods, Michael R. McGowen, Clay Clark, and John Gatesy, 574
Thecadactylus rapicauda, 644
Thecostraca, 931
Thereuonema, 922
Thermodynamic integration, 190
Thermodynamic integration, 675
Thermoplasma, 844, 854
Thermotoga maritima, 855
Theromyzon trizonare, 711
Thomomys bottae, 308–310, 464
Thomomys bulbivorus, 310
Thomomys idahoensis, 310
Thomomys mazama, 310
Thomomys monticola, 310
Thomomys talpoides, 309, 310
Thomomys townsendii, 300, 307, 309, 310
Thomomys umbrinus, 300, 308, 310
Thomomys, 294–298, 300, 302, 305–310, 518, 886, 889
Thomomys. Geomyidae, 294
Thoracobombus, 68
Thoracosaurus, 181
Thouinia, 796
Thouinopsis, 796
Three-interval data set, 288
Thul, 934
Thuliana:genes, 930, 936
Thulina stephaniae, 923
Thulina, 934
Thulinia stephaniae, 922
Thulinia, 925, 927, 930, 934
Thulinia:genes, 934
Tigriopus californicus, 644
Time dependency, 730
tk3, 274
tn, 672
TNT, 234
Tolpis, 744, 745, 747, 748
Tomocerus, 922
Tonina cinereovirens, 143
Toona, 798
Topological score, 613
  as a function of the Robinson-Foulds, 618, 619
  relationship between the Kuhner-Felsenstein distance, 618
  distribution of, 619, 620
  as a function of gene size for the 246 individual gene phylogenies, 622
Topology proposals, 86
Topology, 785
  result for the star, 788
  frequency of, 789

Townsend, Ted M., see Wiens, John J., 420
Townsendii, 310
Toxoneuron, 940
Trachyboa, 429
Trachyiulus nordquisti, 922
Tragopogon, 56
Tragulus napu, 33
Trebouxia, 156
Tree bisection reconnection (TBR), 20, 42, 60, 78, 90
Tree of life, 613, 835
Tree-based methods, 450
Trees of Trees: An Approach to Comparing Multiple Alternative Phylogenies, Tom M. W. Nye, 785
Tretodictyum, 391, 395, 396, 398
Trichoderma reesei, 615
Trichopeziza, 156
Trichoplax, 392, 396
Trifolium, 467, 468, 472, 473
Triggerfish
  global diversification rate of, 909
  age and evolutionary history of, 906
Trigona, 60, 74, 75, 947
Trigonella, 466–470, 473, 476, 480
Triguera, 747
Trilophosuchus rackhami, 180
Triops longicaudatus, 922
Triops, 925, 927, 929
Tripleurospermum, 280
Triseriata, 552
trn, 272, 274, 276, 283, 284, 733, 808
trnA, 41
trnC-ycf6, 704
trnD-trnT, 796
trnI, 41
trnL, 41, 796
trnL-F, 55, 796
trnL-trnF, 704
trnN, 41
trnR, 41
trnT-trnD, 704
trnT-trnF, 55
trnV, 41
Trochodendron, 39
Trogloglanis pattersoni, 117, 128
Tropicalis, 537
Tropidophis, 429
tubB, 489
Tubulosum, 391
Turdus feae, 258
Turdus iliacus, 264
Turdus, 257–259, 261, 263–266, 268
Turdus, 257
Tursiops truncatus, 588
Tursiops, 30, 589
Two-interval data set, 288
Typhlomolge, 514
Typhonium giganteum, 279
Typhonium, 272, 276
Typhonodorum, 277
Tyrrhenoleuctra, 283
UA, 648, 649
Ukurunduense, 805
Ultrametric, 828
Ultrametric, 540
Ungaliophis, 429
Units of co-occurrence, 432
  and clustering coefficient, 437, 438
  extracting, 438, 439
Uroleucon, 463
Uropeltis melanogaster, 429
Uropeltis, 424, 429
Urosaurus, 172
Ursus arctos, 509
Usnea, 142
Ustilago maydis, 615
V-nigra, 568
Vacoparis, 514
Vagrans, 235
Valdiviae, 391
Van de Peer, Yves, see Baele, Guy, 675
Van der Mark, Paul, see Lakner, Clemens, 86
Vansteelandt, Stijn, see Baele, Guy, 675
Variation distance, 249
Venditti, Chris, Meade, Andrew, and Pagel, Mark, Phylogenetic Mixture Models Can Reduce Node-Density Artifacts, 286
Veronica cymbalaria, 365
Veronica, 329
Vicariance, 4, 693
  basic rationale of, 12
  pattern of, 5
Vidua, 464
Vincelestes neuquenianus, 316
Viola palmensis, 747
Virginianus, 880, 886
Virginianus, 885
Visciworous, 261
Vitellinus, 720, 721, 724, 728
Vitis, 39, 41, 55
Vorona, 195, 196
Vultur gryphus, 512
VWF, 500, 501
W. leuckarti, 398
Wagner and Dollo: A Stochastic Duet by Composing Two Parsimonious Solos, Alexander V. Alekseyenko, Christopher J. Lee, and Marc A. Suchard, 772
Wagner, Warren L., see Clark, John R., 693
Wahlberg, Niklas, and Wheat, Christopher West, Genomic Outposts Serve the Phylogenomic Pioneers: Designing Novel Nuclear Markers for Genomic DNA Extractions of Lepidoptera, 231
Walking legs, 646
Walteria leuckarti, 398
Walteria, 391, 395, 398, 402
Wardiana, 796
Weapons, 857
Web site, 613
Web-based taxonomy, 661
Wedin, Mats, see Ekman, Stefan, 141
Wehe, Andre, see Sanderson, Michael J., 335
Whale, 15
Wheat, Christopher West, see Wahlberg, Niklas, 231
Whitfield, James B., Cameron, Sydney A., Huson, Daniel H. and Steel, Mike A., Filtered Z-Closure Supernetworks for Extracting and Visualizing Recurrent Signal from Incongruent Gene Trees, 939
Wiens, John J., Kuczynski, Caitlin A., Smith, Sarah A., Mulcahy, Daniel G., Sites Jr., Jack W., Townsend, Ted M., and Reeder, Tod W., Branch Lengths, Support, and Congruence: Testing the Phylogenomic Approach with 20 Nuclear Loci in Snakes, 420
Wikipedia, 822
Willerslev, Eske, see Munch, Kasper, 750
Wills, Matthew A., Barrett, Paul M. and Heathcote, Julia F., The Modified Gap Excess Ratio (GER*) and the Stratigraphic Congruence of Dinosaur Phylogenies, 891

WIN, 404
Wingless, 87, 241, 289
Withania aristata, 280
Wolseley 18/2/98, 143
Woody clade, 53
WRF, 763, 764
WRF-SBS/WRF-RBS, 767
Wörheide, Gert, see Dohrmann, Martin, 388
X. auromarginatus, 912
X. ringens, 912
Xanthichthys auromarginatus, 906, 907
Xanthichthys mento, 907
Xanthichthys ringens, 907
Xanthichthys, 906, 912, 916
Xanthosoma, 272
Xantusia vigilis, 421
Xantusia, 645
Xenobalistes, 907
Xenodermus, 430
Xenopeltis, 429
Xenophidion schaeferi, 430
Xenopus leavis, 342
Xenopus tropicalis, 521
Xenopus, 537
Xerophilus, 310
Xiphosura, 931
Xlox, 708, 712, 714, 715
Xvaria, 468
Yanornis, 188, 189, 192, 193
Yarrowia lipolytica, 615
ycf1, 41, 42
ycf15, 41
ycf2, 41
ycf6-psbM, 704
Yee, Danny, On Evolution, 184
Yixianornis grabaui, 200
Yixianornis, 187–189, 192, 193, 198
Yoshida, R., see Schardl, C. L., 483
Yucca moths, 84
Yule tree, 654
Z. cameronensis graueri, 260
Z. citrina innotata, 260
Z. crossleyi, 260
Z. dauma aurea, 260
Z. dixoni, 260
Z. erythronota mendeni, 260
Z. monticola, 260
Z. princei batesi, 260
Z. schistacea, 260
Z. sibirica davisoni, 260
Zaglossus, 175
Zea maize, 478
Zea mays, 747
Zea, 480, 482
Zeus, 533, 538
Zhang, A. B., Sikes, D. S., Muster, C., and Li, S. Q., Inferring Species Membership Using DNA Sequences with Back-Propagation Neural Networks, 202
Zhang, Guanyang, see Meier, Rudolf, 809
Zhang, Louxin, see Li, Guoliang, 628
Ziphirostrum, 873
Ziphius cavirostris, 34, 860, 863, 873, 874
Ziphius, 864, 872
ZooTaxa, 663
Zoothera, 260
Zwick, Andreas, see Regier, Jerome C., 920
Zwickl, Derrick J., see Heath, Tracy A., 160
Zygogeomys trichopus, 450
Zygorhiza kochii, 20, 34
Zygorhiza, 22